

STIC-Biotech/ChemLib

124324

From: Kaushal, Sumesh
Sent: Thursday, June 10, 2004 10:41 AM
To: STIC-Biotech/ChemLib
Subject: 09734672: Interference and Sequence search

mej

09734672: Interference and Sequence search

Please search

- SEQ ID NO:3 1-5711 DNA
- SEQ ID NO:3 120-5708 DNA.

Thanks

S. Kaushal

AU1636, REM2.B85

Ph: 571-27-20769

Mail Box: REM2.C70

- Enpn, Enpn each file removed - SK

RECEIVED
JUN 10 2PM
(STIC)

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: *6/10/04*
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH: *✓*
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: *01/04*
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 11, 2004, 17:45:31 ; Search time 12866 Seconds

(without alignments)
12972.154 Million cell updates/sec

Title: US-09-734-672A-3_COPY_120_5708

Perfect score: 5589

Sequence: 1 ATGGATTATCTGCTCTTCG.....AGATCCCCACAGCCACTAC 5589

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: em_estba:*

2: em_esthum:*

3: em_estm:*

4: em_estm:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_esti:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vxl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1950.8	35.1	2091	11	BC012577 Homo sapi
2	1955	35.0	2090	11	BC030969 Homo sapi
3	1416.4	25.3	1578	11	BC038947 Homo sapi
4	941	16.8	1919	11	AK086173 Mus muscu

5	863	15.4	962	13	BQ068830
6	841.4	15.1	1089	12	BM452288
7	811.8	14.5	845	9	AUI122476
8	760.2	13.6	783	9	AUI142729
9	750.6	13.4	789	14	CK000353
10	746.4	13.4	933	13	BUI171200
11	738.8	13.2	743	12	BG681276
12	701.2	12.5	739	14	CF121736
13	688	12.3	702	9	AUI125312
14	686.6	12.3	739	10	BF508987
15	686.4	12.3	987	12	BM600251
16	666.6	11.9	899	13	BQ422380
17	658.6	11.8	900	10	BF791668
18	631	11.3	631	14	CB155501
19	619.4	11.1	856	13	BUI147444
20	617.6	11.1	921	12	BG178466
21	616.2	11.0	878	13	BQ215100
22	603.8	10.8	630	9	AI592040
23	591.4	10.6	627	9	AI589028
24	591	10.6	724	9	AI915085
25	591	10.6	800	10	BF794879
26	590	10.6	906	13	BQ878445
27	590	10.6	909	13	BQ676829
28	590	10.6	922	13	BUI194336
29	590	10.6	933	13	BQ683955
30	587	10.5	747	12	BG777447
31	583	10.4	947	13	BQ679749
32	579.8	10.4	949	13	BUI155689
33	578	10.3	910	13	BQ677666
34	577.4	10.3	941	13	BUI163307
35	575	10.3	602	10	BE043993
36	561.6	10.0	938	12	BQ257190
37	560.4	10.0	675	9	AL704228
38	545.2	9.8	638	12	EM0042282
39	541.8	9.7	546	14	CB118225
40	535.2	9.6	638	10	BE264293
41	530	9.5	563	10	AM295197
42	528.6	9.5	585	10	AM968546
43	528	9.4	528	14	CB158976
44	516.4	9.2	566	10	AM968720
45	498.2	8.9	509	10	AM504244

ALIGNMENTS

RESULT 1	BC012577	Homo sapiens, clone IMAGE:3996658, mRNA.	2101 bp	mRNA	linear	HTC 04-MAR-2003
LOCUS	BC012577	Homo sapiens, clone IMAGE:3996658, mRNA.				
DEFINITION	BC012577	Homo sapiens, clone IMAGE:3996658, mRNA.				
ACCESSION	BC012577.1	GI:15214876				
VERSION	BC012577.1	GI:15214876				
KEYWORDS	HTC.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1	(bases 1 to 2101)				
AUTHORS	Strausberg, R.					
TITLE	Direct Submission					
JOURNAL	Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA					
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov					
COMMENT	Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: CLONTECH Laboratories, Inc. DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) http://www.systembiology.org contact: amadan@systembiology.org					

Anup Madan, Jessica Fahey, Erin Helton, Mark Ketterman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 19 Row: a Column: 18

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6552298

This clone has the following problem: retained intron.

FEATURES

Location/Qualifiers

1..2101

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3996658"

/tissue_type="Bladder, carcinoma"

/clone_lib="NIH MGC_53"

/lab_host="DH103"

/note="Vector: pDNR-LIB"

ORIGIN

Query Match 35.1%; Score 1960.8; DB 11; Length 2101;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1965; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ATGGAATATATCTCTCTGGGTCGAGTACAAAGTACAAATGTCAATATGCTATGACAGAA 60

Db 124 ATGGAATATATCTCTCTGGGTCGAGTACAAAGTACAAATGTCAATATGCTATGACAGAA 183

Qy 61 ATCTTAGAGTGCCTATCTGCTGAGTGTATCAAGGAACCTGCTCCACAAAGTGTGAC 120

Db 184 ATCTTAGAGTGTCCCATCTGCTGAGTGTATCAAGGAACCTGCTCCACAAAGTGTGAC 243

Qy 121 CACATATTTTGCATATTTGCAATCTTCTCAAACGAGAAAGGCGCTTCACAG 180

Db 244 CACATATTTTGCATATTTGCAATCTTCTCAAACGAGAAAGGCGCTTCACAG 303

Qy 181 TGCTCTTATGTAGAAATGATATACCAAGAGGCGCTTACAGAAAGTACAGATTTAGT 240

Db 304 TGCTCTTATGTAGAAATGATATACCAAGAGGCGCTTACAGAAAGTACAGATTTAGT 363

Qy 241 CAACCTGTGTAGAGCTATTTGAAATCATTTTGTGCTTTTTCAGCTTTGACACAGGTTTGGAG 300

Db 364 CAACCTGTGTAGAGCTATTTGAAATCATTTTGTGCTTTTTCAGCTTTGACACAGGTTTGGAG 423

Qy 301 TATGCAAAACAGCTATATTTTGCAAAAGAGAAATTAATCTCTCTGAACATCTAAAGAT 360

Db 424 TATGCAAAACAGCTATATTTTGCAAAAGAGAAATTAATCTCTCTGAACATCTAAAGAT 483

Qy 361 GAAGTTTCTATCATCCAAAGTATGGCTTACAGAAACCGTGCACAAAGACTTCTACAGAGT 420

Db 484 GAAGTTTCTATCATCCAAAGTATGGCTTACAGAAACCGTGCACAAAGACTTCTACAGAGT 543

Qy 421 GAACCCGAAAATCTCTTCCTGAGGAAACCGAGTCTCAGTGTCCAACTCTCTAAACCTTGGGA 480

Db 544 GAACCCGAAAATCTCTTCCTGAGGAAACCGAGTCTCAGTGTCCAACTCTCTAAACCTTGGGA 603

Qy 481 ACTGTGAGAACTCTGAGGACAAAGCAGGCGATACAACTCAAGAGCGTCTGTCTACATT 540

Db 604 ACTGTGAGAACTCTGAGGACAAAGCAGGCGATACAACTCAAGAGCGTCTGTCTACATT 663

Qy 541 GAATTTGGATCTGATTCTTCTGAAGATACCGTATTAATAGGCAACTTATTTGAGTGTGGGA 600

Db 664 GAATTTGGATCTGATTCTTCTGAAGATACCGTATTAATAGGCAACTTATTTGAGTGTGGGA 723

Qy 601 GATCAGAAATTTGTACAAATCACCCCTCAAGAACCCAGGATGAATCAGTTTGGATTCT 660

Db 724 GATCAGAAATTTGTACAAATCACCCCTCAAGAACCCAGGATGAATCAGTTTGGATTCT 783

Qy 661 GCAGAAAGGCTGCTGTGCAATTTTCTGAGAGCGATGTAAACAAATATCTGAACATCAAA 720

Db 784 GCAGAAAGGCTGCTGTGCAATTTTCTGAGAGCGATGTAAACAAATATCTGAACATCAAA 843

Qy 721 CCCAGTAATATGATTTTGAACACCCACTGGAAGCGTGCAGCTGAGAGGCATCCAGAAAAG 780

Db 844 CCCAGTAATATGATTTTGAACACCCACTGGAAGCGTGCAGCTGAGAGGCATCCAGAAAAG 903

Qy 781 TATCAGGGTATGTTCTGTTTCAAACTTGCATGTGAGGCATGTGGCACAAAATCTCATGCC 840

Db 904 TATCAGGGTATGTTCTGTTTCAAACTTGCATGTGAGGCATGTGGCACAAAATCTCATGCC 963

Qy 841 AGCTCATTTACAGCATGAGAAACAGCAGTTTATTACTACTAAAGACAGAAATGAATGTAGAA 900

Db 964 AGCTCATTTACAGCATGAGAAACAGCAGTTTATTACTACTAAAGACAGAAATGAATGTAGAA 1023

Qy 901 AAGCTGAATTTCTGTATAAAAGCAACAGCCTGGCTTGTAGAGAGCCCAACATAACAGA 960

Db 1024 AAGCTGAATTTCTGTATAAAAGCAACAGCCTGGCTTGTAGAGAGCCCAACATAACAGA 1083

Qy 961 TGGCTGGAAGTAAAGAAACATGTATGATAGCGGACTCCAGCAGACAGAAAAAAGGTA 1020

Db 1084 TGGCTGGAAGTAAAGAAACATGTATGATAGCGGACTCCAGCAGACAGAAAAAAGGTA 1143

Qy 1021 GATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGAAATGGAATAGCAGAAACTGCCATGC 1080

Db 1144 GATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGAAATGGAATAGCAGAAACTGCCATGC 1203

Qy 1081 TCAGAGANTCCTAGAGTACTGGAAGTGTCTTGTGATACACTTAATATAGCAGATTTCAG 1140

Db 1204 TCAGAGANTCCTAGAGTACTGGAAGTGTCTTGTGATACACTTAATATAGCAGATTTCAG 1263

Qy 1141 AAAGTTAATCAGTGGTGTTCAGAGAGTGAATGTAATGTTAGGTTCTGATGACTCACATGAT 1200

Db 1264 AAAGTTAATCAGTGGTGTTCAGAGAGTGAATGTAATGTTAGGTTCTGATGACTCACATGAT 1323

Qy 1201 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTTATGAGCGTTCTAAATAGAGTAGAT 1260

Db 1324 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTTATGAGCGTTCTAAATAGAGTAGAT 1383

Qy 1261 GAATATTTCTGTTTCTCAGAGAAAAATAGACTTACTGGCCAGTGTATCTCATGAGGCTTTA 1320

Db 1384 GAATATTTCTGTTTCTCAGAGAAAAATAGACTTACTGGCCAGTGTATCTCATGAGGCTTTA 1443

Qy 1321 ATATGTAATAAGTGAAGAGTTCACTCCAAATCAGTAGAGAGTAATATTTGAAGACAAATA 1380

Db 1444 ATATGTAATAAGTGAAGAGTTCACTCCAAATCAGTAGAGAGTAATATTTGAAGACAAATA 1503

Qy 1381 TTTGGGAAACCTTATCGGAGAGGCAAGCTCCCACTTAAAGCATGTAATCTGAAAAAT 1440

Db 1504 TTTGGGAAACCTTATCGGAGAGGCAAGCTCCCACTTAAAGCATGTAATCTGAAAAAT 1563

Qy 1441 CTAATTTATAGGAGCATTTGTTTACTGAGCCACAGATAATACAAGAGCGTCCCTCACAAAT 1500

Db 1564 CTAATTTATAGGAGCATTTGTTTACTGAGCCACAGATAATACAAGAGCGTCCCTCACAAAT 1623

Qy 1501 AAATTTAAGGTTAAAGAGACCTACATCAGGCTTCACTCTGAGGATTTTATCAAGAA 1560

Db 1624 AAATTTAAGGTTAAAGAGACCTACATCAGGCTTCACTCTGAGGATTTTATCAAGAA 1683

Qy 1561 GCAGATTTGGCAGTTCAAAAGACTCTCTGAATATGATAAATCAGGGAACCTAACCAAGCGAG 1620

Db 1684 GCAGATTTGGCAGTTCAAAAGACTCTCTGAATATGATAAATCAGGGAACCTAACCAAGCGAG 1743

Qy 1621 CAGATTTGCTCAAGTATGATATTTATCTATATGTTGCTCATGAGAAATTAACAAAAGTGTAT 1680

Db 1744 CAGATTTGCTCAAGTATGATATTTATCTATATGTTGCTCATGAGAAATTAACAAAAGTGTAT 1803

Qy 1681 TCTATTTCAGAAATGAGAAAAATCTTAACCAATAGAAATCACTCCAAAAGAAATCTGCTTTC 1740

Db 1804 TCTATTTCAGAAATGAGAAAAATCTTAACCAATAGAAATCACTCCAAAAGAAATCTGCTTTC 1863

Qy 1741 AAAAAAGGCTGAACTTATTAAGCAGCATATTAAGCAATATGGAATCTCGAATTAATATC 1800

Db 1864 AAAAAAGGCTGAACTTATTAAGCAGCATATTAAGCAATATGGAATCTCGAATTAATATC 1923

Qy 1801 CACAATTTCAAAACCACTTAAAAAGATAGGCTGAGGAGGAGTCTTCTTACACGCAATATT 1860

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124  CACAAATTCACAAAGCACCTAAAGAAATAGGCTGAGGAGGAGTCTCTTACCAGCATATT 1983
1861  CATGGCGTTGACCTAGTACTAGTACGAGAAATCTAAGCCCACTAATGTACTGAAATGCAA 1920
1984  CATGGCGTTGACCTAGTACTAGTACGAGAAATCTAAGCCCACTAATGTACTGAAATGCAA 2043
1921  ATTGATAGTTGTTCTAGCAGTGAAGAGATAGAAAGAAAAAAGTACACCAAA 1972
2044  ATTGATAGTTGTTCTAGCAGTGAAGAGATAGAAAGAAAAAAGTACACCAAA 2095

RESULT 2
BC030969
LOCUS      2090 bp      mRNA      linear      HTC 13-JUN-2002
DEFINITION Homo sapiens, Similar to breast cancer 1, early onset, clone
            IMAGE:4804551, mRNA.
ACCESSION BC030969.1 GI:21411299
VERSION    BC030969.1
KEYWORDS   HTC.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Rukavota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 2090)
            Strausberg, R.
            Direct Submission
            Submitted (03-JUN-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK     NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgabs-remail.nih.gov
            Tissue Procurement: DCTD/DRP
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA 94305
            Web site: http://www-shgc.stanford.edu
            Contact: (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
            R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 41 Row: p Column: 11
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6552298
This clone has the following problem: frame shifted.

FEATURES             Location/Qualifiers
     source           1..2090
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4804551"
                     /tissue_type="Prostate, adenocarcinoma."
                     /clone_lib="NIH_MGC_60"
                     /lab_host="DH10B"
                     /note="vector: pDNR-Lib"

ORIGIN
Query Match      35.08; Score 1955; DB 11; Length 2090;
Best Local Similarity 99.58; Pred. No. 0;
Matches 1961; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY      1  ATCGATTATCTGCTCTTCGCGTTGAAGAAAGTACAAATGTCATTAATGCTATGCGAGAA 60
DB      120  ATCGATTATCTGCTCTTCGCGTTGAAGAAAGTACAAATGTCATTAATGCTATGCGAGAA 179
QY      61  ATCTTAGAGTGTCCCTCTCTGCGTTCATCAAGGACCTCTCTCCCAAGATGTGAC 120
DB      180  ATCTTAGAGTGTCCCTCTCTGCGTTCATCAAGGACCTCTCTCCCAAGATGTGAC 239

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QY      121  CACATATTTTGCAGATGCTGAAACTTCTCAACGAGAGAAAGGGCTTCCACAG 180
DB      240  CACATATTTTGCAGATGCTGAAACTTCTCAACGAGAGAAAGGGCTTCCACAG 239
QY      181  TGTCCCTTTATGTAAAGATGATATAACCAAAAGGAGCCTACAAAGAAAGTACGAGATTAGT 240
DB      300  TGTCCCTTTATGTAAAGATGATATAACCAAAAGGAGCCTACAAAGAAAGTACGAGATTAGT 359
QY      241  CAACTTGTGAGAGCTATTTGAAATCATTTCTGCTTTTTCAGCTTCACACAGGTTGGAG 300
DB      360  CAACTTGTGAGAGCTATTTGAAATCATTTCTGCTTTTTCAGCTTCACACAGGTTGGAG 419
QY      301  TATGCAAAACAGCTATAATTTTCAAAAAGGAAAAATTAACCTCTCCTGAAACATCTTAAAGAT 360
DB      420  TATGCAAAACAGCTATAATTTTCAAAAAGGAAAAATTAACCTCTCCTGAAACATCTTAAAGAT 479
QY      361  GAACTTTCTATCATCCAAAGATGCGGTACAGAAACCGTGCAGAAAGACTTCTACAGACT 420
DB      480  GAACTTTCTATCATCCAAAGATGCGGTACAGAAACCGTGCAGAAAGACTTCTACAGACT 539
QY      421  GAACCGAAAAATCCTTCTTCAGAGAAACAGCTCTCAGTGTCCAACTCTCTAACTTTGGA 480
DB      540  GAACCGAAAAATCCTTCTTCAGAGAAACAGCTCTCAGTGTCCAACTCTCTAACTTTGGA 599
QY      481  ACTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCTCAAAAGACGTCTGTCTACAT 540
DB      600  ACTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCTCAAAAGACGTCTGTCTACAT 659
QY      541  GAACTGGGATCTGATTTCTCTCAAGATACCGTTTAAATAGGCAACTTATTGCGAGTGGGA 600
DB      660  GAACTGGGATCTGATTTCTCTCAAGATACCGTTTAAATAGGCAACTTATTGCGAGTGGGA 719
QY      601  GATCAAGAAATTTTACAAATCAACCCCTCAAGGAAACAGGATGAATCATGTTGGATTCT 660
DB      720  GATCAAGAAATTTTACAAATCAACCCCTCAAGGAAACAGGATGAATCATGTTGGATTCT 779
QY      661  GCAGAAAGCGCTCTGTGGAATTTCTGAGAGCGGATGTAAACAATCTCAACATCATCAA 720
DB      780  GCAGAAAGCGCTCTGTGGAATTTCTGAGAGCGGATGTAAACAATCTCAACATCATCAA 839
QY      721  CCAGTAAATTAATGATTTGAACCACTCTGAGAGAGCGTGACGCTGAGAGGATCCAGAAAAG 780
DB      840  CCAGTAAATTAATGATTTGAACCACTCTGAGAGAGCGTGACGCTGAGAGGATCCAGAAAAG 899
QY      781  TATCAGGCTAGTCTGTGTTCAAACTTCGATGTGGAGCGATGTGGCACAAAATCTCATGCC 840
DB      900  TATCAGGCTAGTCTGTGTTCAAACTTCGATGTGGAGCGATGTGGCACAAAATCTCATGCC 959
QY      841  AGCTCATTAACAGCATGAGAAACAGGAGTTTATTACTCACTTAAAGACAGAAATGATGTAGAA 900
DB      960  AGCTCATTAACAGCATGAGAAACAGGAGTTTATTACTCACTTAAAGACAGAAATGATGTAGAA 1019
QY      901  AAGGCTGAATTTCTGTAATAAAGCAACAGCTGCTTTAGCAAGGAGCGCAACATACAGAG 960
DB      1020  AAGGCTGAATTTCTGTAATAAAGCAACAGCTGCTTTAGCAAGGAGCGCAACATACAGAG 1079
QY      961  TGGGCTGGAGTAAGGAAACATGTAAATGATAGCGGACTCCGACGACAGAAAAAGGTA 1020
DB      1080  TGGGCTGGAGTAAGGAAACATGTAAATGATAGCGGACTCCGACGACAGAAAAAGGTA 1139
QY      1021  GATCTGAATGCTGATCCCTCTGTGTCAGAGAAAGAAATGGAATAAGCAGAAACTGCCATGC 1080
DB      1140  GATCTGAATGCTGATCCCTCTGTGTCAGAGAAAGAAATGGAATAAGCAGAAACTGCCATGC 1199
QY      1081  TCAGAGAAATCTTAGAGATACGAAAGATGTTCTTCTGTAACACTAAATAGCAGCATTCAG 1140
DB      1200  TCAGAGAAATCTTAGAGATACGAAAGATGTTCTTCTGTAACACTAAATAGCAGCATTCAG 1259
QY      1141  AAAAGTTAATGATGCTGTTTCCAGAAAGTGAATGAATCTTAGGTTCTTGATGACTCAGATGAT 1200
DB      1260  AAAAGTTAATGATGCTGTTTCCAGAAAGTGAATGAATCTTAGGTTCTTGATGACTCAGATGAT 1319

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752 AGCGTCAGCTGAGGAGCATCCAGAAAAGTATCAGGGTAGTCTGTCTTCAAACCTTGCAATG 811
Db |||||
366 AGCGTCAGCTGAGGAGCATCCAGAAAAGTATCAGGGTAGTCTGTCTTCAAACCTTGCAATG 425
Qy |||||
812 TGGAGCCATGCGGACAAATCTCATGCCAGCTCATTTACAGCATGAGAACAGCAGTTTAT 871
Db |||||
426 TGGAGCCATGCGGACAAATCTCATGCCAGCTCATTTACAGCATGAGAACAGCAGTTTAT 485
Qy |||||
872 TACTCACTAAACACAGCAATGAATCTAGAAAAGGCTGAATCTGTATAAAAAGCAACACAGC 931
Db |||||
486 TACTCACTAAACACAGCAATGAATCTAGAAAAGGCTGAATCTGTATAAAAAGCAACACAGC 545
Qy |||||
932 CTGGCTTAGCAAGAGGCCAACATTAACAGATGGCTGGAAAGTGAAGAAACATGTAAATGATA 991
Db |||||
546 CTGGCTTAGCAAGAGGCCAACATTAACAGATGGCTGGAAAGTGAAGAAACATGTAAATGATA 605
Qy |||||
992 GCGGAGCTCCAGACACAGAAAAGGTAGATCTGAATGCTGATGCCCTGGTGAGAGAA 1051
Db |||||
606 GCGGAGCTCCAGACACAGAAAAGGTAGATCTGAATGCTGATGCCCTGGTGAGAGAA 665
Qy |||||
1052 AAGAATGGAATPAGCAGAAACTGCCATGCTCAGAGAAATCCTAGAGATACCTGAAGATGTTT 1111
Db |||||
666 AAGAATGGAATPAGCAGAAACTGCCATGCTCAGAGAAATCCTAGAGATACCTGAAGATGTTT 725
Qy |||||
1112 CTTGGAATAACACTAAATAGCAGCAATCAGAAAGTGAATGCTGATGCCCTGGTGAGAGAA 1171
Db |||||
726 CTTGGAATAACACTAAATAGCAGCAATCAGAAAGTGAATGCTGATGCCCTGGTGAGAGAA 785
Qy |||||
1172 AACTGTTAGGTTCTGATGACTCACATGATGGGAGTCTGAATCAAAATGCCAAAGTAGCTG 1231
Db |||||
786 AACTGTTAGGTTCTGATGACTCACATGATGGGAGTCTGAATCAAAATGCCAAAGTAGCTG 845
Qy |||||
1232 ATGTAATGAGAGCTTCTAAATGAGGTAGATGAATATCTGTTCTTCAGAGAAATAGACT 1291
Db |||||
846 ATGTAATGAGAGCTTCTAAATGAGGTAGATGAATATCTGTTCTTCAGAGAAATAGACT 905
Qy |||||
1292 TACTGGCAGTGATCTCATGAGCTTTAATATCTAAAAGTGAAGAGTTTCACTCCAAAT 1351
Db |||||
906 TACTGGCAGTGATCTCATGAGCTTTAATATCTAAAAGTGAAGAGTTTCACTCCAAAT 965
Qy |||||
1352 CAGTAGAGATTAATTTGAAGACAAAATATTTGGAAAACCTATTCGAAGAAGCAAGCC 1411
Db |||||
966 CAGTAGAGATTAATTTGAAGACAAAATATTTGGAAAACCTATTCGAAGAAGCAAGCC 1025
Qy |||||
1412 TCCCACTTAAGCCATGTAAGTAAATCTTAATTTAGGAGCAATTTGTTACTGGCCAC 1471
Db |||||
1026 TCCCACTTAAGCCATGTAAGTAAATCTTAATTTAGGAGCAATTTGTTACTGGCCAC 1085
Qy |||||
1472 AGATAATACAGAGCGTCCCTCCAAATAAATTAAGCCGTAAAAGGAGACCTACATCAG 1531
Db |||||
1086 AGATAATACAGAGCGTCCCTCCAAATAAATTAAGCCGTAAAAGGAGACCTACATCAG 1145
Qy |||||
1532 GCCTTCATCTGAGGATTTATCAGAAAGCAGATTTGGCAGTTCAAAAGACTCCTGAAA 1591
Db |||||
1146 GCCTTCATCTGAGGATTTATCAGAAAGCAGATTTGGCAGTTCAAAAGACTCCTGAAA 1205
Qy |||||
1592 TGATAAATCAGGAACTAAACCAACCGAGCAGATGTCGAATGATGAATTAATTAATA 1651
Db |||||
1206 TGATAAATCAGGAACTAAACCAACCGAGCAGATGTCGAATGATGAATTAATTAATA 1265
Qy |||||
1652 GTGTCTATGAGATTAACCAAAAGGTGATTTATTCAGATGAGAAAATCCTAACCCAA 1711
Db |||||
1266 GTGTCTATGAGATTAACCAAAAGGTGATTTATTCAGATGAGAAAATCCTAACCCAA 1325
Qy |||||
1712 TAGAATCACTCGAAGAGATCTGCTTCAAAACGAAAGCTGACCTATAGCAGCAGTA 1771
Db |||||
1326 TAGAATCACTCGAAGAGATCTGCTTCAAAACGAAAGCTGACCTATAGCAGCAGTA 1385
Qy |||||
1772 TAAGCAATATGGAATCGAATTAATATCCAAATTCAAAAGCACTTAAAAGAAATAGGC 1831
Db |||||
1386 TAAGCAATATGGAATCGAATTAATATCCAAATTCAAAAGCACTTAAAAGAAATAGGC 1445
Qy |||||
1832 TGAGAGAGAGTCTTCTTACAGGCAATTAATCATGGCTTGAACTAGTAGTAGTAGAATC 1891

1446 TGAGGAGGAGTCTTCTTACAGGCAATTCATCGCTTGAACCTAGTAGTCAGTAGAATC 1505
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1892 TRAGCCCACTTAATCTTACTGTAATTCGAATTCGAATTCGATGTTCTTACGAGTGAAGATTA 1951
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Qy |||||
1952 AGAAAAAAA 1961
Db |||||
1566 AAAAAAAA 1575
Qy |||||

RESULT 4
AK086173 1919 bp mRNA linear HTC 20-SEP-2003
LOCUS Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched
DEFINITION library, clone:D930010H15 product:brest cancer 1, full insert
sequence.
ACCESSION AK086173.1 GI:26103274
VERSION HTC; CAP trapper.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20493374
PUBMED 11042153
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujitake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Okazaki, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Kazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Inotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohmoto, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,

Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 41-45-503-9222,
Fax: 41-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.

FEATURES
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evidence: BLASTN, 99%, match=1499)
putative"

misc_feature
209..1919

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Best Local Similarity 73.8%; Pred. No. 4.5e-198;
Matches 1343; Conservative 0; Mismatches 365; Indels 113; Gaps 7;
QY 1 ATGGATTATCTGCTTCGGGTTGAAGAAGTACAAAATGTCATTAAATGCTATGCAGAAA 60
DB 209 ATGGATTATCTGCGCTCAAAATTCAGAGATACAAAATGTCATTAAATGCTATGCAGAAA 268
QY 61 ATCTTAGAGTGCCATCTGTGGAGTTGATCAAGGAACCTGTCTCCAAAAGTGTGAC 120
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QY 121 CACATATTTGCAATTTTGCATGCTGAACCTTCTCAACCAAGAAAGGGGCTTCACAG 180
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QY 181 TGTCTTTATGTAAGAATGATATAACCAAGGAGCCTACAGAAAGTACGAGATTTAGT 240
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QY 421 GAACCGGAATCTCTCTTCCAGGAACAGCTCTCAGTGTCCAACTCTCTAACTTGA 480
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QY 481 ACTGTGAGAACTCTGAGGACAAAGCAGGAGATACAACTCAAAAGACGCTCTGTCTACATT 540
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QY 1381 TTTGGAAAAACCTATCCGAGAGGCAAGCCTCCCAACTTTAAGCCATGTAACCTGAAAAAT 1440
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Qy	1678	GATTTCTATTCAGAAATGAGAAAAATCTTAAACCAATAGAAATCATCTCGAAAAAGAAATCTGCT	1737		
Db	1779	AGTAATCTCCAGAAAGAGAAAAGCGCTCATCCCACTGAATCATTTGAGAAAGGAACTGCT	1838		
Qy	1738	TTCAAAACGAAAGCTGCAACCTATAAGCAGCAGTATAGCAATATGGAATCGAAATTAAT	1797		
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RESULT 5	BQ068830	962 bp	mRNA	linear	EST 02-APR-2002
LOCUS	AGENCOURT 6740238	NIH_MGC_47	Homo sapiens	cDNA clone	IMAGE:5802685
DEFINITION	5', mRNA Sequence.				
ACCESSION	BQ068830				
VERSION	BQ068830.1	GI:19897888			
KEYWORDS	EST.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens (human)				
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 962)				
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-re@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LICM2037 row: h column: 14 High quality sequence stop: 700. Location/Qualifiers i. 962 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5802685" /tissue_type="neuroblastoma, cell line" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH_MGC_47" /note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."				
FEATURES	source				
ORIGIN					
Query Match	15.4%	Score 863;	DB 13;	Length 962;	
Best Local Similarity	96.3%	Pred. No. 8.4e-181;			
Matches 891;	Conservative 0;	Mismatches 32;	Indels 2;	Gaps 1;	
Qy	4332	TCCAGAACAAAGCACATCAGAAAAAGCAGTATTAACTTCAGAAAAAGTAGTGAATACCC	4391		

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (Bases 1 to 1089)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: ceapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

plate: LLAM12200 row: k column: 19

High quality sequence stop: 667.

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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2 kb. Library constructed by Life
Technologies."

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Query Match 15.1%; Score 841.4; DB 12; Length 1089;
Best Local Similarity 96.0%; Pred. No. 5.4e-176;
Matches 928; Conservative 0; Mismatches 31; Indels 8; Gaps 6;
QY 1806 TTCAAAGCACCTAAACAAATAGCTGAGGAGGAGTCTTACACGACATATTCATGC 1865
DB 13 TTCAAAGCACCTAAACAAATAGCTGAGGAGGAGTCTTACACGACATATTCATGC 72
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DB 971 AACGAAA 977

RESULT 7

AUI22476
LOCUS AUI22476 MAMMA1 Homo sapiens cDNA clone MAMMA1002447 5', mRNA
DEFINITION AUI22476 sequence.
ACCESSION AUI22476
VERSION AUI22476.1 GI:10937746
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1. (Bases 1 to 845)
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
Yanamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
Ishigai, T.
HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kiearazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
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TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kiearazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
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Best Local Similarity 99.1%; Pred. No. 2e-169;
Matches 836; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

Qy 3700 GTAACCAATATACCTTCTAGTCTTACTAGCATAAGCACCGTCTGCTACCGAGTCTGTCT 3759
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Qy 3820 GTAATATTTGCAAGGATCTCAGGAAATCATCCTTAGTGAAGAAACAAATGTTCTGCT 3879
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Db 181 AGCTGTTTCTTCAAGTGGATTTGAAGATTTGAAGATTTGAAGATTTGAAGATTTGAAGAT 240

Qy 3940 GATCCTTTCTTGAAGTCTTCTCAAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTT 3999
Db 241 GATCCTTTCTTGAAGTCTTCTCAAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTT 300

Qy 4000 GGCTGAGTCAAGAGAAATTTGTTTCAAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAA 4059
Db 301 GGCTGAGTCAAGAGAAATTTGTTTCAAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAA 360

Qy 4060 AATAATCAAG 4119
Db 361 AATAATCAAG 420

Qy 4120 AGTGAAACAAAGCGTCTCTGAAGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAG 4179
Db 421 AGTGAAACAAAGCGTCTCTGAAGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAG 480

Qy 4180 ACTCAGCAGAGGATACCATGACATGACATGACATGACATGACATGACATGACATGACATG 4239
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Qy 4360 GTATTAACTTCAAGAGAGAGTGTGATATACCTTAAGCCAGATCCAGAGGCTTTCT 4419
Db 661 GTATTAACTTCAAGAGAGAGTGTGATATACCTTAAGCCAGATCCAGAGGCTTTCT 720

Qy 4420 GCTGACAAAGTTTGAAGTGTCTGAGATAGTCTTACCAAGTAAATTAAGAACAGGA -G 4477
Db 721 GCTGACAAAGTTTGAAGTGTCTGAGATAGTCTTACCAAGTAAATTAAGAACAGGAAGT 780

Qy 4478 TGGAAAGGTCA -TCCCTTCTAAATGCCATCATAGATAGTGTGATAGTGTGATAGTGTGAT 4536
Db 781 TGGAAAGGTCAATCCCTTCTAAATGCCATCATAGATAGTGTGATAGTGTGATAGTGTGAT 840

Qy 4537 TGCT 4540
Db 841 TGCT 844

RESULT 8
AUI42729
LOCUS
DEFINITION AUI42729 y79A1 Homo sapiens cDNA clone y79A1000792 5', mRNA
ACCESSION AUI42729
VERSION AUI42729.1 GI:11004250
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; cDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
FEATURES
Location/Qualifiers
1..783
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ORIGIN
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Best Local Similarity 99.1%; Pred. No. 5.6e-158;
Matches 773; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy 3460 TTAGATGATGGTGAATAAGGAAGATAGTCTGCTGAAATTCACATTTAGGAAAGT 3519
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Qy 3520 TCTGCTGTTTTAGCAAAAGCGTCCAGAGAGAGAGCTTAGCAGGAGTCTAGCCCTTTC 3579
Db 61 TCTGCTGTTTTAGCAAAAGCGTCCAGAGAGAGAGCTTAGCAGGAGTCTAGCCCTTTC 120

Qy 3580 ACCATACACATTTGGCTCAGGTTTACCGAAGAGGGGCCAAGAAATAGAGTCTCAGAA 3639
Db 121 ACCATACACATTTGGCTCAGGTTTACCGAAGAGGGGCCAAGAAATAGAGTCTCAGAA 180

Qy 3640 GAGAACTTATCTAGTGAAGATGAAGAGCTTCCCTGCTTCCACACTTGTATTGGTAA 3699
Db 181 GAGAACTTATCTAGTGAAGATGAAGAGCTTCCCTGCTTCCACACTTGTATTGGTAA 240

Qy 3700 GTAAACAATATACCTTCTCAGTCTACTAGGCAATAGCACCGTCTGCTACCGAGTCTGTCT 3759
Db 241 GTAAACAATATACCTTCTCAGTCTACTAGGCAATAGCACCGTCTGCTACCGAGTCTGTCT 300

Qy 3760 AAGAACACAGAGAGAGATTTATATCATCTCAAGAGATAGCTTAATAGCTCAGCTACACCGAG 3819
Db 301 AAGAACACAGAGAGAGATTTATATCATCTCAAGAGATAGCTTAATAGCTCAGCTACACCGAG 360

Qy 3820 GTAATATTTGCAAGGATCTCAGGAAATCATCCTTAGTGAAGAAACAAATGTTCTGCT 3879
Db 361 GTAATATTTGCAAGGATCTCAGGAAATCATCCTTAGTGAAGAAACAAATGTTCTGCT 420

Qy 3880 AGCTGTTTCTTCAAGTGGATTTGAAGATTTGAAGATTTGAAGATTTGAAGATTTGAAGAT 3939
Db 421 AGCTGTTTCTTCAAGTGGATTTGAAGATTTGAAGATTTGAAGATTTGAAGATTTGAAGAT 480

Qy 3940 GATCCTTTCTTGAAGTCTTCTCAAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTT 3999
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Qy 4000 GGCTGAGTCAAG 4059

Db 541 GGTCTGATGTAAGGAATTGGTTTCAGATGATGAGAGAGAGACGGGCTTGGAGAA 600
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 QY 4179 CACTCAGCAGAGGATACCATCAACATTAACCTGATAAAGCTCCAGCAGGAATGGCTGA 4238
 Db 721 CACTCAGCAGAGGATACCATCAACATTAACCTGATAAAGCTCCAGCAGGAATGGCTGA 780

RESULT 9
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 LOCUS AGENCOURT 16368380 NIH_MGC_220 Homo sapiens cDNA clone EST 26-NOV-2003
 DEFINITION IMAGE:30706752 5', mRNA sequence.

ACCESSION CK000353.1 GI:38526387
 VERSION
 KEYWORDS
 SOURCE EST.
 ORGANISM Homo sapiens (human)

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 789)
 NIH-MGC <http://mgs.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics

National Cancer Institute / NIH
 Bldg 31 Rm10A07 Bethesda, MD 20832
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: James Martin, University of Iowa
 cDNA Library Preparation: M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILLNL at:
<http://image.llnl.gov>

Plate: NDAMI070 row: e column: 01
 High quality sequence stop: 713.

Location/Qualifiers

FEATURES

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 /note="Organ: mixed; Vector: pYX-Asc; Site: 1: EcoRI;
 Site 2: NotI; Library is oligo-dT primed and directionally
 cloned denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated with
 EcoR I adaptor, digested with Not I and then cloned
 directionally into pYX-Asc vector. Average insert size
 0.5-1kb. Adaptors 5'(AATTCGACGAGG)3' and 5'd
 (CTGTGTCGG)3'. 3' Linker sequence - GCGCGCTGAGAGCC T18.
 Sequencing primers 3'end: T3 promoter primer 5'd
 (AATACCTCTACTAAGGA)3', 5' End: T7 promoter primer 5'd
 (AATACCTCTACTAAGGA)3'. Library was constructed in the
 laboratory of M. Bento Soares. Average insert size 3-4kb
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 13.4%; Score 750.6; DB 14; Length 789;
 Best Local Similarity 99.3%; Pred. No. 7.7e-156;

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QY	3126	CAATATTAATGAAGTAGTGGTTCAGTACTAATGAAGTGGGCTCCAGTATTAATGAATAGG								3185
Db	65	CAATATTAATGAAGTAGTGGTTCAGTACTAATGAAGTGGGCTCCAGTATTAATGAATAGG								124
QY	3186	TTCCAGTGATGAAGAAACATTTCAACGCACTAGTGTAGAAACAGAGGGCCAAATTTGAATGC								3245
Db	125	TTCCAGTGATGAAGAAACATTTCAACGCACTAGTGTAGAAACAGAGGGCCAAATTTGAATGC								184
QY	3246	TATGCTTAGATTAGGGGTTTTCGAACTGAGGCTTATAAACAAGTCTTCTCTGGAAGTAA								3305
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Db	245	TTGTAAGCATCTTGAATTAATAAAGCAAGATATGAGAGTAGTTCAGACTGTTTAATAC								304
QY	3366	AGATTCTCTCCATATCTGATTTTCAGATACTTAGAACAGCCTATGCGAAGTAGTCATGC								3425
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QY	3486	TACTAGTTTGTCTGAAATACATTAAGGAAAGTTCTGCTGTTTTTTAGCAAAAACGCTCA								3545
Db	425	TACTAGTTTGTCTGAAATACATTAAGGAAAGTTCTGCTGTTTTTTAGCAAAAACGCTCA								484
QY	3546	GAGAGGAGCTTAGCAGGAGTCTTAGCCCTTCCACCATACACATTTGGCTCAGGCTTA								3605
Db	485	GAGAGGAGCTTAGCAGGAGTCTTAGCCCTTCCACCATACACATTTGGCTCAGGCTTA								544
QY	3606	CCGAGAGGGGCCAAGAAATTAGAGTCTCTCAGAGAGAACTTATCTAGTGAGGATGAAGA								3665
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QY	3666	GCTTCCCTGCTTCCAAACATTTGTTATTTGGTAAAGTAAACAATATACCTTCTAGCTAC								3725
Db	605	GCTTCCCTGCTTCCAAACATTTGTTATTTGGTAAAGTAAACAATATACCTTCTAGCTAC								664
QY	3726	TAGCCATAGACCCCTTCTACCGAGTCTGTCTTAAGAACACAGAGGAGATTTATTATC								3785
Db	665	TAGCCATAGACCCCTTCTACCGAGTCTGTCTTAAGAACACAGAGGAGATTTATTATC								724
QY	3786	ATTGAAGATAGCTTAATGACTGCAGTAACCCAGTAAATTTGGCAAAG 3834								
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RESULT 10
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 LOCUS AGENCOURT 7956206 NIH_MGC_72 Homo sapiens cDNA clone EST 04-SEP-2002
 DEFINITION 5', mRNA sequence.
 BUI71200
 VERSION BUI71200.1 GI:22685184
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 933)

NIH-MGC <http://mgs.nci.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC/DCTD/DP	
cDNA Library Preparation: Life Technologies, Inc.	
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
DNA Sequencing by: Agencourt Bioscience Corporation	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	
Plate: LLAM13514 row: C column: 21	
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Best Local Similarity 98.3%; Pred. No. 6.8e-155;	
Matches 765; Conservative 0; Mismatches 11; Indels 2; Gaps 1;	
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Qy	4650 ATCTTACTTCCAGGCAAGATCTAGAGGAACCCCTTACTCGGAATCTGGAATCAGCCT 4709
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Qy	4710 CTCTCTGATGACCTGAATCTGATCCTCTGAGGACAGAGCCCGAGTCAGTCTGT 4769
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Db	312 AAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 371
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Qy	5010 AAAACACACATCACTTTTAACTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5069
Db	432 AAAACACACATCACTTTTAACTAATTAATTAATTAATTAATTAATTAATTAATTAAT 491
Qy	5070 AACAGATGCTGAGTTTGTGTGTGAACGACACTGAAATATTTTCTAGGAATTCGGGAGG 5129
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Qy	5130 AAAATGGGTAGTTAGCTATTCTGGGTGACCCAGTCTATTAAAGAAAGAAATTCGTGAA 5189
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Qy	5190 TGACATGATTTTGAAGTCAGAGGAGATGTGGTCAATGGAGAAACCAACCAAGTCCAAA 5249
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Tissue Procurement: ATCC/DCTD/DP	
cDNA Library Preparation: Life Technologies, Inc.	
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
DNA Sequencing by: Agencourt Bioscience Corporation	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	
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High quality sequence stop: 672.	
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Best Local Similarity 99.7%; Pred. No. 3.2e-153;	
Matches 740; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy	4605 GGAGCAACAGCTGGAGAGTCTGGGCCACACGATTTCAGGAAACATCTTACTTGCACAG 4664
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Qy	4665 GCAGATCTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4724
Db	61 GCAGATCTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
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Db	181 TTCACTCTGATTTGAAAGTTCCCAATTTGAAAGTTGAGATCTGCCAGGTCAGC 240
Qy	4845 TGCCTGCTCATCTACTGATCTGCTGGGTATATGCAATGGAGAAAGTGTGAGCGAGGA 4904
Db	241 TGCCTGCTCATCTACTGATCTGCTGGGTATATGCAATGGAGAAAGTGTGAGCGAGGA 300

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QY 4965 TGGCTGACCCCAAGAAATTTATGCTCGTGTACAGTTTGCAGAAACACCAACATCAC 5024
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QY 5025 TTTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACT 5084
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QY 5085 TGTGTGTGAACGACACTGAAATTTTCTAGGAAATTTGCGGAGGAAATTTGGGTAGTTAG 5144
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QY 5145 CTATTTCTGGTGACCCAGCTCTATTAAGAAAGAAATTTCTGATGATGATGATGATGATG 5204
Db |||||||
QY 5205 AGTCAGAGGAGATGTGTCAATGAAGAAACCAACAGGCTCCAAAGCGAGCAAGAAATC 5264
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QY 721 GCCCACAGATCAACTGGAATGG 742
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CF121736
LOCUS
DEFINITION
IMAGE:30566859 5', mRNA sequence.
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VERSION
KEYWORDS
SOURCE
ORGANISM
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1 (bases 1 to 739)
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MBBRP, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Louis Staudt
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/humanfl.html
Seq primer: PYX-5,
Location/Qualifiers
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DEFINITION
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Constructed from size fractionated cytoplasmic mRNA
(4.4-7.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Patima Bonaudo, Ph.D. and M. Bento Soares, Ph.D."
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ORIGIN

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Matches 720; Conservative 0; Mismatches 14;
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Db 6 GGAGACCCCAAGATCTCATGTTAACTGGAGAAAGGGTTTGCACAACTGAAAG-TCGTGA 64
QY 2293 GAGAGTAGCAGTATTTCACTCTGTTACTGTTATGTTGTTGTTGTTGTTGTTGTTGTTG 2352
Db 65 GAGAGTAGCAGTATTTCACTCTGTTACTGTTATGTTGTTGTTGTTGTTGTTGTTGTTG 124
QY 2353 TTACTCGGAGTTAGCACTCTAGGAGGCAAAACAGAAACCAATATAATGTGTGAGTCAG 2412
Db 125 TTACTCGGAGTTAGCACTCTAGGAGGCAAAACAGAAACCAATATAATGTGTGAGTCAG 184
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QY 2833 AGTATCAAGGAGGCTCTAGGTTTGTCTATCATCTCTAGTTCAGAGGCAACGAACTGGA 2892
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Db 665 CTCATTACTCCAAATAAACAATGACATTTTACAAAACCCATATCGTATACCACTTTT 724
QY 2953 CCCATCAAGTCATTT 2967
Db 725 TCCATCAAGTCATTT 739
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ACCESSION      AUI25312
VERSION        AUI25312.1  GI:10950028
SOURCE         EST
ORGANISM       Homo sapiens (human)

REFERENCE      1 (bases 1 to 702)
AUTHORS       Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J.,
              Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S. and
              Isogai, T.
TITLE         HRI human cDNA project (Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S.,
              Saito, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T.,
              Suzuki, Y., Sugano, S., Isogai, T.)
JOURNAL        Unpublished (2000)
COMMENT       Contact: Takao Isogai
              Genomics Laboratory
              Helix Research Institute
              1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
              Tel: 81-438-52-3975
              Fax: 81-438-52-3986
              Email: genomics@hri.co.jp
              HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
              Research Institute; cDNA library construction: Department of
              Virology, Institute of Medical Science, University of Tokyo, and
              Helix Research Institute.

FEATURES       source
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                precursor cells"

ORIGIN
Query Match      12.3%; Score 688; DB 9; Length 702;
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Matches 699; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Qy 3882 CTGTGTTTCTTCAGTGCAGTGATTTGGAGACTTGCACTGCAAAATCAAAACCCAGGA 3941
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Qy 3942 TCCCTTCTTGATTCGTTCTTCCAAACAAATGAGGCATCGCTGTAAGCCAGGAGTTGG 4001
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RESULT 14
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LOCUS
DEFINITION
BF508987
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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IMAGE:3085787 3', mRNA sequence.
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BF508987.1 GI:11592285
EST.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA library preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
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POLYA-yes
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is a subtracted library derived from NCI_CGAP_Sub5. The
NCI_CGAP_Sub8 library had 2.5 million recombinants. A
single-stranded DNA preparation of NCI_CGAP_Sub5 was used
as a tracer in a subtractive hybridization with a driver
comprising a pool of clones from NCI_CGAP_Sub5 (IMAGE
clone ids 2732833-2737415, 3068040-3069191, 25% of the
driver population), a pool of clones from NCI_CGAP_Sub4
(IMAGE clone ids 2723592-2729326, 25% of the driver
population), NCI_CGAP_Sub6 (pool A19-AJU, IMAGE ids
2728969-2733190, 25% of the driver population), and
NCI_CGAP_Sub7 (IMAGE ids 3069192-3072238,
3081864-3084550, 25% of the driver population).
Subtraction was performed as previously described
[Bonaldo, Lennon & Soares (1996): Normalization and
Subtraction: Two Approaches To Facilitate Gene Discovery.
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Genome Research 6, 791-806.
TAG_SEQ=None found"

ORIGIN

Query Match 12.3%; Score 686.6; DB 10; Length 739;
Best Local Similarity 99.1%; Pred. No. 1.3e-141;
Matches 689; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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RESULT 15
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BM800251
VERSION
BM800251.1 GI:19117074
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SOURCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 987)
AUTHORS
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: AFCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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FEATURES

Location/Qualifiers

ORIGIN

Query Match 12.3%; Score 686.4; DB 12; Length 987;
Best Local Similarity 85.8%; Pred. No. 1.5e-141;
Matches 874; Conservative 0; Mismatches 14; Indels 131; Gaps 5;
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QY 819 ATGTGGCACAATCTATCTCCAGCTCATTTACAGCATGAGAAACAGCAGTTTATTACTCAC 878
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Job time : 12875 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 11, 2004, 17:57:55 ; Search time 336 Seconds
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Capext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1
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; Sequence 5, Application US/08798691
; Patent No. 5750400
; GENERAL INFORMATION:
; APPLICANT: Murphy, Patricia D.
; APPLICANT: Allen, Antonette C.
; APPLICANT: Alvares, Christopher P.
; APPLICANT: Critz, Brenda S.
; APPLICANT: Olson, Sheri J.
; APPLICANT: Schelter, Denise B.
; APPLICANT: Zeng, Bin
; TITLE OF INVENTION: Coding Sequences of the Human
; TITLE OF INVENTION: BRCA1 Gene
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSER: ONCORMED
; STREET: 200 Perry Parkway
; CITY: Gaithersburg
; STATE: MD
; COUNTRY: USA
; ZIP: 20877

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,691
FILING DATE: 12-Feb-97
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Thomas Gallegos
REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: PA-0054CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-527-2651
TELEFAX: 301-208-6997
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRAINEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORGANISM: Homo sapiens
STRAIN: BRCA1
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17

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Sequence 10, Appl
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Sequence 10, Appl
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Sequence 9, Appli

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DB	1500 TTTGGGAAACCTTATCGGAGAGAGGCAAGCTCCCAACTTAAAGCATGTAACTGAAAT	1559
QY	1441 CTAAATATAGAGCATTTGTTTACTGAGCCACAGATAATCAAGAGCGTCCCTCCACAAAT	1500
DB	1560 CTAAATATAGAGCATTTGTTTACTGAGCCACAGATAATCAAGAGCGTCCCTCCACAAAT	1619
QY	1501 AAATTAAGGCTTAAAGGAGCACTTACATGAGGCTTCTCTGAGGATTTTATCAGAAA	1560
DB	1620 AAATTAAGGCTTAAAGGAGCACTTACATGAGGCTTCTCTGAGGATTTTATCAGAAA	1679
QY	1561 GCAGATTTGGCAGTTCAAAAGACTCTCTGAAATGATTAATCAGGGAATCAACCAAGCGAG	1620
DB	1680 GCAGATTTGGCAGTTCAAAAGACTCTCTGAAATGATTAATCAGGGAATCAACCAAGCGAG	1739
QY	1621 CAGATGCTCAAGTGAATATTAATTAATGAGTGTCTCATGAGAAATAAACAAGGATGAT	1680
DB	1740 CAGATGCTCAAGTGAATATTAATTAATGAGTGTCTCATGAGAAATAAACAAGGATGAT	1799
QY	1681 TCTATTCAGAAATGAGAAAAATCTTAACCAATAGAACTCACTCGAAAAAGAAATCTGCTTTC	1740
DB	1800 TCTATTCAGAAATGAGAAAAATCTTAACCAATAGAACTCACTCGAAAAAGAAATCTGCTTTC	1859
QY	1741 AAAACGAAGCTGAACCTATAGCAGCAGTATAGCAATATGGAATCTGGAATTTAAATATC	1800
DB	1860 AAAACGAAGCTGAACCTATAGCAGCAGTATAGCAATATGGAATCTGGAATTTAAATATC	1919
QY	1801 CAGATTTCAAAAGCACTTAAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCATATT	1860
DB	1920 CAGATTTCAAAAGCACTTAAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCATATT	1979
QY	1861 CATGCGCTTCAACTAGTAGTCAATCTAGAAATCTAAGCCCACTAATTTGATCTGAATTCGAA	1920
DB	1980 CATGCGCTTCAACTAGTAGTCAATCTAGAAATCTAAGCCCACTAATTTGATCTGAATTCGAA	2039
QY	1921 ATTGATAGTTGTTCTAGCAGTGAAGATAAAGAAAAAAGTACACCAAAATGCCAGTC	1980
DB	2040 ATTGATAGTTGTTCTAGCAGTGAAGATAAAGAAAAAAGTACACCAAAATGCCAGTC	2099
QY	1981 AGGCACAGCAGAAACCTTCAAACTCATGGAAGTAAAGAACTTGCCTGAGGCGCAAGAG	2040
DB	2100 AGGCACAGCAGAAACCTTCAAACTCATGGAAGTAAAGAACTTGCCTGAGGCGCAAGAG	2159
QY	2041 AGTAAACGCAATGAACAGACAGATTAAGACATGACAGTGTACTTTTCCAGAGCTG	2100
DB	2160 AGTAAACGCAATGAACAGACAGATTAAGACATGACAGTGTACTTTTCCAGAGCTG	2219

Qy	1	ATGGAATTAATCTGCTCTTTCGCGTGTGAAGAGTACAAAATGTTCATTAATGCTATGCAGAA	60
Db	120	ATGGAATTAATCTGCTCTTTCGCGTGTGAAGAGTACAAAATGTTCATTAATGCTATGCAGAA	179
Qy	61	ATCTTAGAGTGTCCCATCTGTGTGTGGAGTTGATCAAGGAACTGTCTCCCAAAAGTGTGAC	120
Db	180	ATCTTAGAGTGTCCCATCTGTGTGTGGAGTTGATCAAGGAACTGTCTCCCAAAAGTGTGAC	239
Qy	121	CACATATTTTGGCAAAATTTTGTGCCTGCTGAAACTTCTCAACGAGAGAAAGGGCTTCCACAG	180
Db	240	CACATATTTTGGCAAAATTTTGTGCCTGCTGAAACTTCTCAACGAGAGAAAGGGCTTCCACAG	299
Qy	181	TGTCCTTTATGTAAAGATGATATAACGAAAGGAGGCTACAGAAAGTACAGATTTAGT	240
Db	300	TGTCCTTTATGTAAAGATGATATAACGAAAGGAGGCTACAGAAAGTACAGATTTAGT	359
Qy	241	CAACTTGTGCAAGAGCTATTGAAATCAATTTGTGCTTTTTCAGCTTGACACAGCTTTGGAG	300
Db	360	CAACTTGTGCAAGAGCTATTGAAATCAATTTGTGCTTTTTCAGCTTGACACAGCTTTGGAG	419
Qy	301	TATGCAAAACGCTATAATTTTGCMAAAAGGAAATAAATCTCTCTGAAATCTTAAAGAT	360
Db	420	TATGCAAAACGCTATAATTTTGCMAAAAGGAAATAAATCTCTCTGAAATCTTAAAGAT	479
Qy	361	GAGTTTCTATCATCCAAAGATGTGGCTACAGAAAACGTCGCCAAAAGACTTCTTACAGAT	420
Db	480	GAGTTTCTATCATCCAAAGATGTGGCTACAGAAAACGTCGCCAAAAGACTTCTTACAGAT	539
Qy	421	GAAACCCGAAATCGCTTCGTGAGGAAACCAAGTCTCAGTGTCCAACTCTCTTAACCTTGA	480
Db	540	GAAACCCGAAATCGCTTCGTGAGGAAACCAAGTCTCAGTGTCCAACTCTCTTAACCTTGA	599
Qy	481	ACTGTGAGAACTGTGAGGACAAAGCAGCGGATACAACTCTCAAAAGACGTCGTGCTACATT	540
Db	600	ACTGTGAGAACTGTGAGGACAAAGCAGCGGATACAACTCTCAAAAGACGTCGTGCTACATT	659
Qy	541	GAAATGGGATCTGATTTCTGTGAAGATACCGTTTAATAAGGCAACTTATTGCAAGTGTGGGA	600
Db	660	GAAATGGGATCTGATTTCTGTGAAGATACCGTTTAATAAGGCAACTTATTGCAAGTGTGGGA	719
Qy	601	GATCAAGAAATGTTTACAAATCAACCCCTCAAGAACCAAGGATGAAATCAGTTTGGATTCT	660
Db	720	GATCAAGAAATGTTTACAAATCAACCCCTCAAGAACCAAGGATGAAATCAGTTTGGATTCT	779
Qy	661	GCAAAAAGCGTGTGTGTGAAATTTTCTGAGACGGATGTAAACAAATCTGAACATCATCAA	720
Db	780	GCAAAAAGCGTGTGTGTGAAATTTTCTGAGACGGATGTAAACAAATCTGAACATCATCAA	839
Qy	721	CCGAGTAATATGATTTGAAACACCACTGAGNAGCGTCAGCTGAGGGCATCCAGAAAG	780
Db	840	CCGAGTAATATGATTTGAAACACCACTGAGNAGCGTCAGCTGAGGGCATCCAGAAAG	899
Qy	781	TATCAGGATAGTTCTGTTTCAAACTTGCACTGTGAGGCCATGTGSCACAAATATCTCATGCC	840
Db	900	TATCAGGATAGTTCTGTTTCAAACTTGCACTGTGAGGCCATGTGSCACAAATATCTCATGCC	959
Qy	841	AGCTCATTTACAGATGAGAACAGCAGTTTATTACTTCACTAAGACAGATGATGTAGAA	900
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Qy	901	AAGGCTGAATTTCTGTAAATAAAGCAAAACAGCGCTGGCTTAGCAAGGAGCAACATTAACAGA	960
Db	1020	AAGGCTGAATTTCTGTAAATAAAGCAAAACAGCGCTGGCTTAGCAAGGAGCAACATTAACAGA	1079
Qy	961	TGGGCTGGAAGTAAGGAACCATGTAAATGATAGGCGGACTCCACGACAGAAAAAAGGTA	1020
Db	1080	TGGGCTGGAAGTAAGGAACCATGTAAATGATAGGCGGACTCCACGACAGAAAAAAGGTA	1139
Qy	1021	GATCTGAATGCTGATCCCTCTGTGTGAGAGAAAAGAAATGGAATTAAGCAGAAACTGCCATGC	1080
Db	1140	GATCTGAATGCTGATCCCTCTGTGTGAGAGAAAAGAAATGGAATTAAGCAGAAACTGCCATGC	1199
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1260	AAAGTTAATGAGTGGTGTTCAGAGAGTGAAGAACTGTTAGGTTCCTGATCACTCACATGAT	1319
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1320	GGGGAGCTCGAATCAAAATGCCAAAGTAGCTGATGTAATTTGGAGGTCTCTAAATGAGGTAGAT	1379
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1380	GAATATTTCTGGTCTTTTCAGAGAAAATAGACTTTACTGGCCAGTGAATCCTCATGAGGCTTTA	1439
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1440	ATATGTAAGAAGTGAAGAGGTTCACTCCAAATCAGTAGAGAGTAAATTTGAAGACAAAAATA	1499
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1500	TTTGGGAAACCTTATCGGAAGAGGCAAGCCTCCCCAACTTAAGCCATGCTAACTGAAAAAT	1559
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1560	CTAATTTATAGGAGCATTTGTTACTCTGAGCCACAGATAAATCAAGAGCGTCCCTCTCAAAAT	1619
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1680	GCAGATTTGCGAGTTCAAAAAGACTCCTGAAATCATAAATCAGGGAACCTAACCCAAACGGAG	1739
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1740	CAGAACTGCTCAAGTAGATGAATATTACTAATAGTGGTCTAGAGAAATAAAACAAAGGTGAT	1799
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1800	TCTAATTCAGAAATGAGAAAAATCCTTAACCCCAATAGAATCACTCGAAAAAGAAATCTGCTTC	1859
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1860	AAAAACGAAGCTGAACCTATAAGCAGCAGGTATTAAGCAATATGGAATCTGAAATTAATATTC	1919
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1920	CACAAATTCBAAGCAGCCCTTAAAGAAATAGCTCAGGAGGAAGTCTTCTACACGACATAT	1979
1861	CATGCGCTTGAACCTAGTAGTCAGTAGAAATCTTAAGCCCACTAATTTGATCTGAATTCGAA	1920
1980	CATGCGCTTGAACCTAGTAGTCAGTAGAAATCTTAAGCCCACTAATTTGATCTGAATTCGAA	2039
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2041	AGTAAACAGCCAAATGAAACAGACAGTAAAGACATGACAGTGAATCTTTCCCGAGCTG	2100
2160	AGTAAACAGCCAAATGAAACAGACAGTAAAGACATGACAGTGAATCTTTCCCGAGCTG	2219
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2220	AGGTAAACAAATGACCTGGTCTTTTACTAAGTGTTCAAATACCAAGTGAACCTTTAAAGAA	2279
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4920 AAGATTCCTCCCAATGGAAGTTCAGAAATCTGCCAGGGTCCAGCTGCTGCTCATACTACT 4979
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5221 GTCAATGGAAGAAACCAACAGGTCCAAAGCGAGCAAGAGAAATCCAGGACAGAAAGATC 5280
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5400 TTCAGGGGCTAGAAATCTGTTGCTATGGCCCTTCCACCAATGCCACAGATCAACTG 5459
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5520 GGCACAGGTGTCCACCAATGTGTGTGTCAGCCAGATGCTGACAGAGGAGCAATGCG 5579
5461 TTCCATGCAATTGGGCAGATGTGTGAGGACACCTGTGTGTCACCCGAGAGTGGGTGTGGAC 5520

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QY 5521 AGTGTAGCACTTACCAAGTCCAGAGTGCACACCTTACCTGATACCCGAGATCCCCCAG 5580
Db 5640 AGTGTAGCACTTACCAAGTCCAGAGTGCACACCTTACCTGATACCCGAGATCCCCCAG 5699
QY 5581 AGCCACTAC 5589
Db 5700 AGCCACTAC 5708

RESULT 4
US-08-598-591-1
; Sequence 1, Application US/08598591
; Patent No. 5654155
; GENERAL INFORMATION:
; APPLICANT: Allen, Antonette C.
; APPLICANT: Alvares, Christopher P.
; APPLICANT: Critz, Brenda S.
; APPLICANT: Murphy Patricia B.
; APPLICANT: Olson, Sheri J.
; APPLICANT: Schelter, Denise B.
; APPLICANT: Zeng, Bin
; TITLE OF INVENTION: A Consensus Sequence of the Human BRCA1 Gene
; Patent No. 5654155
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/598,591
; FILING DATE: herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Swecker, Robert S.
; REGISTRATION NUMBER: 19,885
; REFERENCE/DOCKET NUMBER: 020160-282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; STRAIN: BRCA1
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 17
; MAP POSITION: 17q21
US-08-598-591-1

Query Match 100.0%; Score 5587.4; DB 1; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5588; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCAATTATCTGCTCTTCGGTTGAGAGAGTACAAATCTCATTAATGCTATCCAGAAA 60
Db 120 ATGCAATTATCTGCTCTTCGGTTGAGAGAGTACAAATCTCATTAATGCTATCCAGAAA 179

QY 61 ATCTTAGAGTGTCCATCTGTCTGGAGTGTGATCAAGGAACCTGTCTCCACAAAGTGTGAC 120
DB 180 ATCTTAGAGTGTCCATCTGTCTGGAGTGTGATCAAGGAACCTGTCTCCACAAAGTGTGAC 239
QY 121 CACATATTTTGCATAATTTTGCATGCTGAATCTTCTCAACGAGAAAGAGGCCCTTTCACAG 180
DB 240 CACATATTTTGCATAATTTTGCATGCTGAATCTTCTCAACGAGAAAGAGGCCCTTTCACAG 299
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QY 241 CAATCTGTGTGAAGAGCTATTTGAAATCATTTTGTGCTTTTTCAGCTTGTGACACAGGTTTGGAG 300
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DB 540 GAACCCGAAATCTCTCTGACGAAACCAAGTCTCAGTGTCCAACTCTCTACCTTGGGA 599
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DB 600 ACTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGAGGCTCTGTCTCAAT 659
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DB 660 GAATTTGGATCTGATCTTCTGAAAGATACCGTTTAATTAAGGCACTTATTCAGTGTGGGA 719
QY 601 GATCAAGAAATTTTACAAATCACCCTCAAGGAACCAAGGATGAATCAAGTTTGGATCT 660
DB 720 GATCAAGAAATTTTACAAATCACCCTCAAGGAACCAAGGATGAATCAAGTTTGGATCT 779
QY 661 GCAAAAAGGCTGTCTGGAATTTTCTGAGCGGAATTAACAAATCTGAACTATCATCAA 720
DB 780 GCAAAAAGGCTGTCTGGAATTTTCTGAGCGGAATTAACAAATCTGAACTATCATCAA 839
QY 721 CCCAGTAATATGATTTGACACCACTGAGGAAGGCTGAGGAGGATCCAGAAAG 780
DB 840 CCCAGTAATATGATTTGACACCACTGAGGAAGGCTGAGGAGGATCCAGAAAG 899
QY 781 TATCAGGCTAGTCTGTCTTCAAACTTGCATGTGAGGCCATGTGCGACAAATCTCATGCC 840
DB 900 TATCAGGCTAGTCTGTCTTCAAACTTGCATGTGAGGCCATGTGCGACAAATCTCATGCC 959
QY 841 AGCTCATATCAGCATGAGAACAGCAGTTTATCTACTACTAAGACAGAAATGATGTAGAA 900
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QY 901 AAGGCTGAATCTGTATAAAGCAACAGCCTGGCTTAGCAGGAGCCCAACATACAGA 960
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DB 1080 TGGGCTGGAAGTAAAGGAAACATGTAATGATAGGCGGACTCCAGACAGAAAAAGGTA 1139
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DB 1200 TCAGAGAACTCTAGAGTACTAGAGATGTTCTTGGTAACACTAAATAGCAGCACTTCAG 1259
QY 1141 AAAGTTAATGAGTGGTTTTCCAGAAAGTGAATGAACTGTTAGTGTCTGTGATCACTCATGAT 1200

DB 1260 AAAGTTAATGAGTGGTTTTCCAGAAAGTGAATGAACTGTTAGTTCTGTGATCACTCACATGAT 1319
QY 1201 GGGGAGCTCTGAATCAAAATCCAAAGTAGCTGTGATGTGAGAGCTTCTAAATGAGGTAGAT 1260
DB 1320 GGGGAGCTCTGAATCAAAATCCAAAGTAGCTGTGATGTGAGAGCTTCTAAATGAGGTAGAT 1379
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QY 1621 CAGAAATGCTCAAGTGAATGATTTACTTAATAGTGTGTCATGAGAAATAAACAAGAGGTGAT 1680
DB 1740 CAGAAATGCTCAAGTGAATGATTTACTTAATAGTGTGTCATGAGAAATAAACAAGAGGTGAT 1799
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QY 2041 AGTAACAGCCAAATGAAACAGACAGTAAAGACATGACAGTACTTTCAGAGAGCTG 2100
DB 2160 AGTAACAGCCAAATGAAACAGACAGTAAAGACATGACAGTACTTTCAGAGAGCTG 2219
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DB 2220 AAGTTAAACAAATGCACTGTTCTTTTACTTAAGTGTTCAAATACCAAGTGAACCTTAAAGAA 2279
QY 2161 TTTTCAATCTTAGGCTTCCAAAGAGAGAAAAAGAGAGAACTAGAAACAGTTAAAGTG 2220
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RESULT 6

US-08-825-487A-1

Sequence 1, Application US/08825487A

Patent No. 6048689

GENERAL INFORMATION:

APPLICANT: Murphy, Patricia D.

APPLICANT: White, Marga B.

TITLE OF INVENTION: METHODS FOR IDENTIFYING VARIATIONS IN POLYNUCLEOTIDE

NUMBER OF SEQUENCES: 110

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howrey & Simon

STREET: 1299 Pennsylvania Avenue., N.W.

CITY: Washington,

STATE: DC

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/825,487A

FILING DATE: 28-MAR-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US98/060002

FILING DATE: 26-Mar-1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

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REGISTRATION NUMBER: 25,227

REFERENCE/DOCKET NUMBER: 05371.0012.999

TELECOMMUNICATION INFORMATION:

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INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 5711 base pairs

TYPE: nucleic acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: CDNA

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

STRAIN: BRCA1

POSITION IN GENOME:

CHROMOSOME/SEGMENT: 17

MAP POSITION: 17q21

US-08-825-487A-1

Query Match 100.0%; Score 5587.4; DB 3; Length 5711;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 5588; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 180 ATCTTAGAGTGTCCCATCTCTCTGGAGTTGATCAAGAACCTGTCTCTCCCAAAGTGTGAC 239

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Db 2400 GAAAGATCTGTAGAGTAGCAGTATTTTCACTGCTGATCTGCTGATCTGCTGCTGCTG 2459
Qy 2341 GAAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
Db 2460 GAAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2519

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Db 2520 TGTGTAGTCAGTGTGAGCAATTTGAAACCCCAAGGGACCTAATTTATGTTGTTTCCAAA 2579
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QY 5581 AGCCACTAC 5589
Db 5700 AGCCACTAC 5708

RESULT 7

US-09-074-476-1

Sequence 1, Application US/09074476
Patent No. 6130322
GENERAL INFORMATION:
APPLICANT: Murphy, Patricia D.
APPLICANT: Allen, Antonette C.
APPLICANT: Alvares, Christopher P.
APPLICANT: Critz, Brenda S.
APPLICANT: Olson, Sheri J.
APPLICANT: Thurber, Denise
APPLICANT: Zeng, Bin
TITLE OF INVENTION: Coding Sequences of the Human
NUMBER OF SEQUENCES: 72
TITLE OF INVENTION: BRCA1 Gene
CORRESPONDENCE ADDRESS:
ADDRESSER: Howrey & Simon
STREET: 1299 Pennsylvania Avenue N. W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,476
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/074,453
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 5371.34.US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8109
TELEFAX: 650-463-8400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCA1 (om11)
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
US-09-074-476-1

Query Match 100.0%; Score 5587.4; DB 3; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5588; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 ATCTTAGAGTGTCCCATCTGCTGAGGTGTGATCAAGGAACCTGTCTCCAAAGTGTGAC 120
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RESULT 8

US-10-022-819-1

; Sequence 1, Application US/10022819

; Patent No. 6886163
; GENERAL INFORMATION:
; APPLICANT: ALLEN, Antonette C. P.
; OLSEN, Sheri J.
; LAWRENCE, Tammy
; ANGELLY, Tracy S.
; BABIN, Mark B.
; TITLE OF INVENTION: CODING SEQUENCE HAPLOTYPE OF THE HUMAN
; BRCAL GENE
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan Lewis & Bockius LLP
; STREET: 1111 Pennsylvania Avenue
; CITY: Washington DC
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/022.819
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/074,452
; FILING DATE: 1998-05-06
; ATTORNEY/AGENT INFORMATION:
; NAME: <Unknown>
; REGISTRATION NUMBER: <Unknown>
; REFERENCE/DOCKET NUMBER: 044921-5049-01-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-739-3000
; TELEFAX: 202-739-3001
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; STRAIN: BRCAL
; HAPLOTYPE: OM14
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 17
; MAP POSITION: 17q21
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-022-819-1

Query Match 99.9%; Score 5585.8; DB-4; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5587; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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5581 AGCCACTAC 5589
5700 AGCCACTAC 5708
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RESULT 9

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US-08-798-691-3
; Sequence 3, Application US/08798691
; Patent No. 5750400
; GENERAL INFORMATION:
; APPLICANT: Murphy, Patricia D.
; APPLICANT: Allen, Antonette C.
; APPLICANT: Alvarez, Christopher P.
; APPLICANT: Critz, Brenda S.
; APPLICANT: Olson, Sheri J.
; APPLICANT: Schelter, Denise B.
; APPLICANT: Zeng, Bin
; TITLE OF INVENTION: Coding Sequences of the Human
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ONCORMED
; STREET: 200 Perry Parkway
; CITY: Gaithersburg
; STATE: MD
; COUNTRY: USA
; ZIP: 20877
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,691
; FILING DATE: 12-Feb-97
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas Gallegos
; REGISTRATION NUMBER: 32,692
; REFERENCE/DOCKET NUMBER: PA-0054CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-527-2051
; TELEFAX: 301-208-6997
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; STRAIN: BCRA1
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 17
; MAP POSITION: 17q21
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US-08-798-691-3
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Query Match 99.9%; Score 5581; DB 1; Length 5711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5584; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 300 TGTCTTTTATAGAAATGATATAACCAAGAGGCGCTTCAAGAAAGTACAGAGATTTAGT 359
QY 241 CAACCTTGTGAAGAGCTATTGAAAATCAATTTGTGCTTTTTCAGCTTTGACACAGGTTTGGAG 300
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Db 360 CAACTGTGTGAAGAGCTATTGAAATCATTTGTGCTTTTCAGCTTGAACACAGGTTTGGAG 419
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 Db 480 GAAGTTTCTATCATCAAAAGTATGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAT 539
 Qy 421 GAACCGAAATCTTCTTCAGAGAAACCAAGTCTCAGTGTCCAACTCTCTAACTTGGGA 480
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RESULT 10

US-08-825-487A-3

; Sequence 3, Application US/08825487A

; Patent No. 604689

; GENERAL INFORMATION:

; APPLICANT: Murphy, Patricia D.
; APPLICANT: White, Marga B.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING VARIATIONS IN POLYNUCLEOTIDE SEQUENC
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue., N.W.
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,487A
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/060002
; FILING DATE: 26-Mar-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 05371.0012.999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-463-8100
; TELEFAX: 650-463-8400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; STRAIN: BRCA1
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 17
; MAP POSITION: 17q21
; US-08-825-487A-3

Query Match 99.9%; Score 5581; DB 3; Length 5711;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 5584; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 1800 TCTATTTCA GAAATGAGAAATCTTAACCAATAGATCACTCGAAAAAGAACTCTGCTTTC 1859
QY 1741 AAAACGAA AGCTGAACTTATAGCAGCAGTATAAGCAATATCGNACTCGAATTAATATTC 1800
Db 1860 AAAACGAA AGCTGAACTTATAGCAGCAGTATAAGCAATATCGNACTCGAATTAATATTC 1919
QY 1801 CACAAATTC AAAAGCACCTTAAAAAGAAATAGGCTGAGAGGAAGTCTTTCTACCGAGGCATAT 1860
Db 1920 CACAAATTC AAAAGCACCTTAAAAAGAAATAGGCTGAGAGGAAGTCTTTCTACCGAGGCATAT 1979
QY 1861 CATGGCTT GAACTAGTAGTAGTAGTAGTAATCTAAGCCCACTTAATTTGTAATTTGCA 1920
Db 1980 CATGGCTT GAACTAGTAGTAGTAGTAGTAATCTAAGCCCACTTAATTTGTAATTTGCA 2039
QY 1921 ATTTGATG TGTGTTCTAGCAGTGAAGATATAAGAAAAAGTACAAACCAATGCCAGTC 1980
Db 2040 ATTTGATG TGTGTTCTAGCAGTGAAGATATAAGAAAAAGTACAAACCAATGCCAGTC 2099
QY 1981 AGGCA CAGCAGAAACCTCACTCACTGGAAGGTAAAGAACCTTGCAACTGGAGCCAGAG 2040
Db 2100 AGGCA CAGCAGAAACCTCACTCACTGGAAGGTAAAGAACCTTGCAACTGGAGCCAGAG 2159
QY 2041 AGTAA CAAAGCCAAATGAACAGACAGTAAAGACATGACAGTGATCTTTCCAGAGCTG 2100
Db 2160 AGTAA CAAAGCCAAATGAACAGACAGTAAAGACATGACAGTGATCTTTCCAGAGCTG 2219
QY 2101 AAGTTAA CAAATGCACTGGTCTTTTACTAAGTGTTCATAATACAGTGAACTTTAAAGAA 2160
Db 2220 AAGTTAA CAAATGCACTGGTCTTTTACTAAGTGTTCATAATACAGTGAACTTTAAAGAA 2279
QY 2161 TTTGTCAAT CCTAGCTTCCAGAGAGAAAGAGAGAACTAGAAACAGTTTAAAGTG 2220
Db 2280 TTTGTCAAT CCTAGCTTCCAGAGAGAAAGAGAGAACTAGAAACAGTTTAAAGTG 2339
QY 2221 TCTAATAT GCTGAGAACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTTCGAACT 2280
Db 2340 TCTAATAT GCTGAGAACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTTCGAACT 2399
QY 2281 GAAAGATCT GTGAGAGTAGCAGTATTTTCACTGTGTAACCTGTACTGATTTATGGCACTCAG 2340
Db 2400 GAAAGATCT GTGAGAGTAGCAGTATTTTCACTGTGTAACCTGTGTAACCTGTATTTGCACTCAG 2459
QY 2341 GAAAGTATCT GTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAACCAATATA 2400
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QY 2401 TGTGTGAGT CAGTGTGAGGCAATTTGAAAAACCCCAAGGGACTAATTCATGTGTGTTCGAAA 2460
Db 2520 TGTGTGAGT CAGTGTGAGGCAATTTGAAAAACCCCAAGGGACTAATTCATGTGTGTTCGAAA 2579
QY 2461 GATAATAGA AATGACACAGAGGCTTTAAGTATTCATTTGGGACATGAAGTTTAAACCAAGT 2520
Db 2580 GATAATAGA AATGACACAGAGGCTTTAAGTATTCATTTGGGACATGAAGTTTAAACCAAGT 2639
QY 2521 CGGAAAAA CAGCATAGAAATGGAAGAAAGTGAATCTGATCTCAGTATTTTGCAGAAATACA 2580

Db 2640 CGGGAAACAAGCATAGAAATGGAAGAGTGAACCTTGATGCTCAGTATTTGCAGATACA 2699
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Db 2700 TTCAAGGTTTCAAAGCGCAGTCAATTTCTCTGTTTCAAAATCCAGGAAATGCAGAGAG 2759
Qy 2641 GAATGTGCAACAATTTCTCTGCCACCTCTCGGCTCTTAAAGAACAAAGTCCAAAAGTCACT 2700
Db 2760 GAATGTGCAACAATTTCTCTGCCACCTCTCGGCTCTTAAAGAACAAAGTCCAAAAGTCACT 2819
Qy 2701 TTGTAATCTGAACAAAGGAGAAATCAAGGAAGATGAGTCTTAATATCAAGCCTGTA 2760
Db 2820 TTGTAATCTGAACAAAGGAGAAATCAAGGAAGATGAGTCTTAATATCAAGCCTGTA 2879
Qy 2761 CAGACAGTTAATATCACTCAGGCTTTCTCTGTTGTTGTCAGAAAGATAACCCAGTTGAT 2820
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Qy 2821 AATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGC 2880
Db 2940 AATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGC 2999
Qy 2881 AACGAAACTGGACTCAATTAATCAAAATAAATGAGCTTTTACAAAACCCATATCGTATA 2940
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Qy 2941 CCACCACCTTTTCCCATCAGTCAATTTGTTAAACTAAATGATAGAAATATCTGCTAGAG 3000
Db 3060 CCACCACCTTTTCCCATCAGTCAATTTGTTAAACTAAATGATAGAAATATCTGCTAGAG 3119
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Db 3120 GAAACCTTTGAGGAACATTTCAATGTCACTGAAAGAGAAATGCGAAATGAGAAACATTTCCA 3179
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Qy 3121 TCAAGCAATATTAATGAAGTAGTTTCCAGTACTAATGAAGTGGCTCCAGTATTAATGAA 3180
Db 3240 TCAAGCAATATTAATGAAGTAGTTTCCAGTACTAATGAAGTGGCTCCAGTATTAATGAA 3299
Qy 3181 ATAGGTTCCAGTATGAAACATTTCAAGCAGACTAGGTAGAAACAGAGGCCCAAAATTTG 3240
Db 3300 ATAGGTTCCAGTATGAAACATTTCAAGCAGACTAGGTAGAAACAGAGGCCCAAAATTTG 3359
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Db 3360 AATGCTATGCTTAGGTTAGGGGTTTTGCAACCTGAGGCTTATTAACAAAGTCTTCTCTGGA 3419
Qy 3301 AGTAATTTGTAAGCAATCTGAAATTAAGAAAGCAAGAAATATGAGAAAGTAGTTTCAGACTGTT 3360
Db 3420 AGTAATTTGTAAGCAATCTGAAATTAAGAAAGCAAGAAATATGAGAAAGTAGTTTCAGACTGTT 3479
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Db 3480 AATACAGATTTCTCTCCATATCTGATTTTCAGATTAATCTTAGAACAGCCTATCGGAGTAGT 3539
Qy 3421 CATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGTTGTAATAAG 3480
Db 3540 CATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGTTGTAATAAG 3599
Qy 3481 GAAGATATAGTTTGTCTGAAATGACATTAAGGAAAGTCTCTGCTTTTTTGTAGCAAAAGC 3540
Db 3600 GAAGATATAGTTTGTCTGAAATGACATTAAGGAAAGTCTCTGCTTTTTTGTAGCAAAAGC 3659
Qy 3541 GTCCAGAGAGAGAGCTTAGCAGGAGTCTTAGCCCTTTTACCCATACACATTTTGGCTCAG 3600
Db 3660 GTCCAGAGAGAGAGCTTAGCAGGAGTCTTAGCCCTTTTACCCATACACATTTTGGCTCAG 3719
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Db 3720 GGTTCAGAGAGAGAGAGCTTAGCAGGAGTCTCTCAGAGAGAACTTTATCTAGTGAGGAT 3779
Qy 3661 GAAGAGCTTCCCTGCTCTCCAAACACTTTGTTATTTTGGTAAAGTAAACAATATACCTTCTCAG 3720
Db 3780 GAAGAGCTTCCCTGCTCTCCAAACACTTTGTTATTTTGGTAAAGTAAACAATATACCTTCTCAG 3839
Qy 3721 TCTACTAGGATAGACACCGTTGCTACCGAGTGTCTGTCTTAAGAACACAGAGGAGAAATTTA 3780
Db 3840 TCTACTAGGATAGACACCGTTGCTACCGAGTGTCTGTCTTAAGAACACAGAGGAGAAATTTA 3899
Qy 3781 TTATCATTTGAAGAAATAGCTTTAAATGATGTCAGTAACACAGGTAATATTTGGCAAGGCAATCT 3840
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Qy 3841 CAGGAAACATCACCTTTAGTGAGGAAAACAAAATGTTTCTGTAGCTTGTCTTCCACAGTGC 3900
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Qy 3901 AGTGAATTTGGAAGACTTGACTGCTCAAAATCAAAACCCAGGATCCTTTCTTGAATGGTTCT 3960
Db 4020 AGTGAATTTGGAAGACTTGACTGCTCAAAATCAAAACCCAGGATCCTTTCTTGAATGGTTCT 4079
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Qy 4021 GTTTCAGATGATGAGAAAGAGGAAACGGGCTTGGAAAGAAATTAATCMAGAGAGCAAGC 4080
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Db 4200 ATGGATTTCAAACCTTAGTGAAGCAGCATCTGGGTGTGAGAGTGAACAAGCAAGCTCTCTGAA 4259
Qy 4141 GACTGCTCAGGGCTATCTCTCTCAGAGTGAACATTTTAAACCACTCAGCAGAGGGATACCATG 4200
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Qy 4681 ACCCTTTACTGGAATCTGGAATCAGCTTCTCTGATGACCTCTGATGACCTCTGATGATCTCTCT 4740
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DB 480 GAAGTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCACAAAGACTTCTACAGAGT 539
QY 421 GAACCCGAAATCCTTCCTCCAGGAAACCACTCTCAGTGTCCAACTCTCTAACTTTGGA 480
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QY 481 ACTGTGGAACCTCTGAGGACAAAGCAGCGGATACAACTCTCAAAAGAGCTGTGTCTACATT 540
DB 600 ACTGTGGAACCTCTGAGGACAAAGCAGCGGATACAACTCTCAAAAGAGCTGTGTCTACATT 659
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DB 720 GATCAAGAAATGTTTACAAATCACCCCTCAAGGAACCCAGGGATGAATCAGTTTGGATTCT 779
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DB 1920 CCAATTTCAAAAGCACCTTAAAGAAATAGCTCAGGAGGAAGTCTTCTACAGGCAATT 1979
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Db 4440 GACTGCGGAATTCAGAAACAAAGCAATCAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4499
Qy 4381 AGTGAATACCTTATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4440
Db 4500 AGTGAATACCTTATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4559
Qy 4441 GCAGATAGTCTTACCAAGTAAAGAAACAAAGCAATCAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 4500
Db 4560 GCAGATAGTCTTACCAAGTAAAGAAACAAAGCAATCAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 4619
Qy 4501 TGCCCATCATTAGATGATAGTGTGTATGACAGTGTCTCTGAGGAGGAGGAGGAGGAGGAGGAGG 4560
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Qy 4561 AACTACCCATCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4620
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Qy 4681 ACCGCTTACCTGGAATCTGGAATCAGGCTCTTCTCTGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 4740
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Db 3300 ATAGTTCCTAGTGAGAAACATTCAGCGAATCTAGTGAACAGAGGAGGAGGAGGAGGAGG 3359
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Qy 841 AGCTCATTTACAGCATGAGAACAGCAGTTTATTACTCACTAAAGACAGAAATGATGTAGAA 900
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Qy 5581 AGCCACTAC 5589
|||||

Db 5700 AGCCACTAC 5708
RESULT 14
US-09-099-753-1
; Sequence 1, Application US/09099753
; Patent No. 6149903
; GENERAL INFORMATION:
; APPLICANT: HOLT, JEFFREY T.
; APPLICANT: JENSEN, ROY A.
; APPLICANT: PAGE, DAVID L.
; APPLICANT: KING, MARY-CLAIRE
; APPLICANT: SZABO, CSILLA I.
; APPLICANT: JETTON, THOMAS L.
; APPLICANT: ROBINSON-BENION, CHERYL L.
; APPLICANT: THOMPSON, MARILYN E.
; TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2
; TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON
; TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
; STREET: BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 kB storage
; COMPUTER: IBM PC/XT/AT compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,753
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/603,753
; FILING DATE: 20 FEB 1996
; APPLICATION NUMBER: U.S. 08/373,799
; FILING DATE: 17 JAN 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: ARLES A. TAYLOR, JR.
; REGISTRATION NUMBER: 39,395
; REFERENCE/DOCKET NUMBER: 1242/2
; TELEPHONE: (919) 493-8000
; TELEFAX: (919) 419-0383
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5712
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE: adult
; TISSUE TYPE: female breast
; CELL TYPE: ductal carcinoma in situ, invasive
; CELL TYPE: breast cancer and normal breast tissue
; CELL LINE: not derived from a cell line
; ORGANELLS: no
; IMMEDIATE SOURCE:
; LIBRARY: cDNA library derived from human
; CLONE: obtained using published sequence
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: unknown

MAP POSITION: unknown
UNITS: unknown
FEATURE: unknown
NAME/KEY: BRCA1
LOCATION: GenBank accession no. U14680
IDENTIFICATION METHOD: microscopically directed
IDENTIFICATION METHOD: sampling and nuclease protection assay
OTHER INFORMATION: gene encoding BRCA1 protein
PUBLICATION INFORMATION:
AUTHORS: Miki, Y., et. al.
TITLE: A strong candidate gene for the breast and
ovarian cancer susceptibility gene BRCA1.
JOURNAL: Science
VOLUME: 266
PAGES: 66-71
DATE: 1994
RELEVANT RESIDUES IN SEQ ID NO: 1:
US-09-099-753-1

Query Match 99.8%; Score 5579.4; DS 3; Length 5712;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5583; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGGATTATCTGCTCTCGGTTGAAGAGTCAAAATGTCTAATGCTATGCGAGAA 60
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Db 420 TATGCAACAGCTATATTTTGCAAAAGGAAATTAATCTCTGACATCTAAGAT 479

Qy 361 GAAGTTTCTATCTATCCAAAGTATGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAT 420
Db 480 GAAGTTTCTATCTATCCAAAGTATGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAT 539

Qy 421 GAACCCGAAATCTCTCTTGGAGAAACCGAGTCTAGTGTCAACTCTCTAACTTTGGA 480
Db 540 GAACCCGAAATCTCTCTTGGAGAAACCGAGTCTAGTGTCAACTCTCTAACTTTGGA 599

Qy 481 ACTGTGAGAACTCTGAGCAAAAGCAGCGATCAACCTCAAAAGAGCTCTGCTACATT 540
Db 600 ACTGTGAGAACTCTGAGCAAAAGCAGCGATCAACCTCAAAAGAGCTCTGCTACATT 659

Qy 541 GAATTTGGATCTGATCTTCTGAGATACCGTTTAATAGGCAACTTATTGCAAGTGGGA 600
Db 660 GAATTTGGATCTGATCTTCTGAGATACCGTTTAATAGGCAACTTATTGCAAGTGGGA 719

Qy 601 GATCAGAAATTTGTACAAATCAACCTCAAGGAACGAGGATCAATCAGTTGGATTCT 660
Db 720 GATCAGAAATTTGTACAAATCAACCTCAAGGAACGAGGATCAATCAGTTGGATTCT 779

Qy 661 GCAAAAAGGCTGCTGTGTAATTTCTGACACGATGTAAACAAATCTGAAATCATCAA 720
Db 780 GCAAAAAGGCTGCTGTGTAATTTCTGACACGATGTAAACAAATCTGAAATCATCAA 839

Qy 721 CCCAGTAATTAATTTGAACCACTGAGAAAGCGGTGACCTGAGAGGCAATCCAGAAAG 780
Db 1841 CCCAGTAATTAATTTGAACCACTGAGAAAGCGGTGACCTGAGAGGCAATCCAGAAAG 839

Qy 781 TATCAGGTTAGTTCTGTTTCAAACTTGGCATGTGGAGCCATGTGGCAAAATCTCATGCC 840
Db 900 TATCAGGTTAGTTCTGTTTCAAACTTGGCATGTGGAGCCATGTGGCAAAATCTCATGCC 959

Qy 841 AGCTCATTTACAGCATGAGACACAGCTTTTATCTCACTAAAGACAGAAATGTATGTA 900
Db 960 AGCTCATTTACAGCATGAGACACAGCTTTTATCTCACTAAAGACAGAAATGTATGTA 1019

Qy 901 AAGGCTCAATTTCTGTAATTAAGCAACAGCTGCTGGCTTAGCAAGGACCAACATAACAG 960
Db 1020 AAGGCTCAATTTCTGTAATTAAGCAACAGCTGCTGGCTTAGCAAGGACCAACATAACAG 1079

Qy 961 TGGGCTGGAAGTAAAGCAACATGTAATGATAGGCGGACTCCAGCAGCAAGAAAAGGTA 1020
Db 1080 TGGGCTGGAAGTAAAGCAACATGTAATGATAGGCGGACTCCAGCAGCAAGAAAAGGTA 1139

Qy 1021 GATCTGAATGCTGATCCCTCTGTGTGAGAGAAAGAAATGGAATAGCAGAAACTGCCATGC 1080
Db 1140 GATCTGAATGCTGATCCCTCTGTGTGAGAGAAAGAAATGGAATAGCAGAAACTGCCATGC 1199

Qy 1081 TCAGAGATCTTAGAGATCTGAAGATGTTCTTGTGATTAACACTAAATAGCAGCTTCAG 1140
Db 1200 TCAGAGATCTTAGAGATCTGAAGATGTTCTTGTGATTAACACTAAATAGCAGCTTCAG 1259

Qy 1141 AAAGTTAAATGAGTGGTTTTCAGAGTGTGAATCTGTAGGTTCTGATGACTCACATGAT 1200
Db 1260 AAAGTTAAATGAGTGGTTTTCAGAGTGTGAATCTGTAGGTTCTGATGACTCACATGAT 1319

Qy 1261 GGGAGTCTGAATCAAAATGCCAAAGTGTGATGTAATGGAAGCTTCTAAATAGAGGTAGAT 1260
Db 1320 GGGAGTCTGAATCAAAATGCCAAAGTGTGATGTAATGGAAGCTTCTAAATAGAGGTAGAT 1379

Qy 1261 GAATATTTCTGTTTCTTTCAGAGAAATAGACTTCTAGGCGAGTGTCTCATGAGGCTTTA 1320
Db 1380 GAATATTTCTGTTTCTTTCAGAGAAATAGACTTCTAGGCGAGTGTCTCATGAGGCTTTA 1439

Qy 1321 ATATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGAGTAAATATTGAGCAAAAATA 1380
Db 1440 ATATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGAGTAAATATTGAGCAAAAATA 1499

Qy 1381 TTTGGGAAACCTATCGGAAGAGGCAAGCTCCCACTTAAGCCATCTTAATGAAAT 1440
Db 1500 TTTGGGAAACCTATCGGAAGAGGCAAGCTCCCACTTAAGCCATCTTAATGAAAT 1559

Qy 1441 CTAAATTTAGGAGCAATTTCTTACTGAGCCACAGATAATAAGAGCGTCCCTCACAAT 1500
Db 1560 CTAAATTTAGGAGCAATTTCTTACTGAGCCACAGATAATAAGAGCGTCCCTCACAAT 1619

Qy 1501 AAATTAAGCGTAAAGAGGACCTACATCAGGCTTCTCTGAGGATTTTATCAGAAA 1560
Db 1620 AAATTAAGCGTAAAGAGGACCTACATCAGGCTTCTCTGAGGATTTTATCAGAAA 1679

Qy 1561 GCAGATTTGGCAGTTCAAAAGACTCTGAAATGATTAATCAGGAACTTAACCAAGCGAG 1620
Db 1680 GCAGATTTGGCAGTTCAAAAGACTCTGAAATGATTAATCAGGAACTTAACCAAGCGAG 1739

Qy 1621 CAGATGTTCAAGTCAATGAAATTAATTAATAGTGTCTAGAGAAATAAACAAGAGTGTAT 1680
Db 1740 CAGATGTTCAAGTCAATGAAATTAATTAATAGTGTCTAGAGAAATAAACAAGAGTGTAT 1799

Qy 1681 TCTATTTCAAGATGAGAAATCTTAACCCCAATAGAAATCACTCGAAAAGAAATCTCTTTC 1740
Db 1800 TCTATTTCAAGATGAGAAATCTTAACCCCAATAGAAATCACTCGAAAAGAAATCTCTTTC 1859

Qy 1741 AAAACGAAAGCTGAACCTTAAGCAGCAGTATAGCAATATGGAATCGAATTAATATC 1800
Db 1860 AAAACGAAAGCTGAACCTTAAGCAGCAGTATAGCAATATGGAATCGAATTAATATC 1919

Qy 1801 CACAAATTCAGAGCACTTAAAGAAATAGGCTGAGGAGAGTCTTCTACAGGCAATAT 1860
Db 1920 CACAAATTCAGAGCACTTAAAGAAATAGGCTGAGGAGAGTCTTCTACAGGCAATAT 1979

1861 QY CATGGCTTGAACCTAGTAGTCAGTAGAATCTAAGCCCACTAAATGTTGACTGAATGCCAA 1920
1980 Db CATGGCTTGAACCTAGTAGTCAGTAGAATCTAAGCCCACTAAATGTTGACTGAATGCCAA 2039
1971 QY ATTGATAGTGTCTTACGAGTGAAGATGAAGAAAGAAAGTACCAACCAATGCCAGTC 1980
2040 Db ATTGATAGTGTCTTACGAGTGAAGATGAAGAAAGAAAGTACCAACCAATGCCAGTC 2099
1981 QY AGGCACAGCAAAACCTACAACTCATGGAAGGTAAAGAACTGCACTGGAGCCAAAG 2040
2100 Db AGGCACAGCAAAACCTACAACTCATGGAAGGTAAAGAACTGCACTGGAGCCAAAG 2159
2041 QY AGTACAGCCCAATGACAGCAAGTAAAGACATGACAGTGTATCTTTCCAGAGCTG 2100
2160 Db AGTACAGCCCAATGACAGCAAGTAAAGACATGACAGTGTATCTTTCCAGAGCTG 2219
2101 QY AAGTTAAACAAATGCACCTGTGTTCTTTTACTAAGTGTTCAAATACCACTGAACTTAAAGAA 2160
2220 Db AAGTTAAACAAATGCACCTGTGTTCTTTTACTAAGTGTTCAAATACCACTGAACTTAAAGAA 2279
2161 QY TTTGTCATCTAGCTTCCAGAGAGAGAAAGAGAAACTAGAAACAGTTAAAGTG 2220
2280 Db TTTGTCATCTAGCTTCCAGAGAGAGAAAGAGAAACTAGAAACAGTTAAAGTG 2339
2221 QY TCTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTGCAACT 2280
2340 Db TCTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTGCAACT 2399
2281 QY GAAAGATCTGATAGAGATGAGCAGTATTTCACTGTGTACTGTGTACTGATTTAGCAGCTCAG 2340
2400 Db GAAAGATCTGATAGAGATGAGCAGTATTTCACTGTGTACTGTGTACTGATTTAGCAGCTCAG 2459
2341 QY GAAAGATCTGTTACTGGAAGTTAGCAGCTCTAGGGAAGGCAAAAACAGAACCAATATAA 2400
2460 Db GAAAGATCTGTTACTGGAAGTTAGCAGCTCTAGGGAAGGCAAAAACAGAACCAATATAA 2519
2401 QY TGTGTAGTCACTGTGAGCAATTTGAAACCCCAAGGAGCTAAATTCATGTTGTTCCAAA 2460
2520 Db TGTGTAGTCACTGTGAGCAATTTGAAACCCCAAGGAGCTAAATTCATGTTGTTCCAAA 2579
2461 QY CATTAAGATGATGACAGAGAGCTTTAAGTATCCATGAGACATGAAGTTAACCACT 2520
2580 Db CATTAAGATGATGACAGAGAGCTTTAAGTATCCATGAGACATGAAGTTAACCACT 2639
2521 QY CCGGAAACAAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAAGTATTTGCAATACA 2580
2640 Db CCGGAAACAAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAAGTATTTGCAATACA 2699
2581 QY TTCAAGGTTTCAAAGCCGAGTCAATTTGCTCTGTTTTCAAATCCAGGAATGCAAGAG 2640
2700 Db TTCAAGGTTTCAAAGCCGAGTCAATTTGCTCTCGTTTTCAAATCCAGGAATGCAAGAG 2759
2641 QY GAATGTGCAATTTCTGTCGCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAAGTCACT 2700
2760 Db GAATGTGCAATTTCTGTCGCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAAGTCACT 2819
2701 QY TTTGAATGTGAACAAAAGGAAGAAATCAAGGAAGAAATGAGTCTAATATCAAGCCCTGTA 2760
2820 Db TTTGAATGTGAACAAAAGGAAGAAATCAAGGAAGAAATGAGTCTAATATCAAGCCCTGTA 2879
2761 QY CAGACAGTTAATATCACTGAGGCTTTCTGTTGTTGTCAGGAAGATGAAGCCAGTTGAT 2820
2880 Db CAGACAGTTAATATCACTGAGGCTTTCTGTTGTTGTCAGGAAGATGAAGCCAGTTGAT 2939
2821 QY AATGCCAAATGATATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGC 2880
2940 Db AATGCCAAATGATATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGC 2999
2881 QY AACGAACTGCACTTACTTCCAAATGAACATGAGCTTTTACAAAACCCATATCGTATA 2940
3000 Db AACGAACTGCACTTACTTCCAAATGAACATGAGCTTTTACAAAACCCATATCGTATA 3059

2941 QY CACGACTTTTCCGATCAAGTCAATTTGTTAAAACTAATGTAAAGAAAATCTGCTAGAG 3000
3060 Db CCACCACTTTTCCGATCAAGTCAATTTGTTAAAACTAATGTAAAGAAAATCTGCTAGAG 3119
3001 QY GAAACCTTTGAGGAACATTTCAATGTCACTGCAAGAGAAATGGAATGGAACATTTCCA 3060
3120 Db GAAACCTTTGAGGAACATTTCAATGTCACTGCAAGAGAAATGGAATGGAACATTTCCA 3179
3061 QY AGTACAGTGAAGCAAAATTAGCCGTAATAACATTAAGAAAATGTTTAAAGAGGACGC 3120
3180 Db AGTACAGTGAAGCAAAATTAGCCGTAATAACATTAAGAAAATGTTTAAAGAGGACGC 3239
3121 QY TCAAGCAATATTAATGAAGTGTGCTTCCAGTACTTAATGAAGTGGCTCCAGTATTAATGAA 3180
3240 Db TCAAGCAATATTAATGAAGTGTGCTTCCAGTACTTAATGAAGTGGCTCCAGTATTAATGAA 3299
3181 QY ATAGGTTCCAGTGAATAAACATTTCAAGCAGAACTAGGTAGAAACAGAGGGCCAAAATTG 3240
3300 Db ATAGGTTCCAGTGAATAAACATTTCAAGCAGAACTAGGTAGAAACAGAGGGCCAAAATTG 3359
3241 QY AATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGCTCTATAACAAAAGTCTTCTCGA 3300
3360 Db AATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGCTCTATAACAAAAGTCTTCTCGA 3419
3301 QY AGTAAATTGTAAGCATCTCGAAATFAAAAAGCAAGATATGAAGAGTAGTTCAGACTGTT 3360
3420 Db AGTAAATTGTAAGCATCTCGAAATFAAAAAGCAAGATATGAAGAGTAGTTCAGACTGTT 3479
3361 QY AATACAGATTTCTCTCATATCTGATTTTCAAGATTAAGTACAGCTATGGAGTAGT 3420
3480 Db AATACAGATTTCTCTCATATCTGATTTTCAAGATTAAGTACAGCTATGGAGTAGT 3539
3421 QY CATGCACTCTCAGGTTTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAG 3480
3540 Db CATGCACTCTCAGGTTTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAG 3599
3481 QY GAAGATCTAGTTTTGCTGGAATGAACATTAAGGAAGTTCTGCTGTTTTTAGCAAAAGC 3540
3600 Db GAAGATCTAGTTTTGCTGGAATGAACATTAAGGAAGTTCTGCTGTTTTTAGCAAAAGC 3659
3541 QY GTCCAGAGAGGAGCTTAGCAGGAGTCTTAGCCCTTTTCCACCATACACATTTGGCTCAG 3600
3660 Db GTCCAGAGAGGAGCTTAGCAGGAGTCTTAGCCCTTTTCCACCATACACATTTGGCTCAG 3719
3601 QY GGTACCGAAGAGGGGCCAAGAAAATTAGAGTCTCTAGAGAGAGAACTTATCTAGTAGGAT 3660
3720 Db GGTACCGAAGAGGGGCCAAGAAAATTAGAGTCTCTAGAGAGAGAACTTATCTAGTAGGAT 3779
3661 QY GAAGAGCTTCCCTGCTTCCAACTTTGTTATTTGGTAAAGTAAACAAATATACCTTCTCAG 3720
3780 Db GAAGAGCTTCCCTGCTTCCAACTTTGTTATTTGGTAAAGTAAACAAATATACCTTCTCAG 3839
3721 QY TCTACTAGGCATAGCAACCTTGTACCGAGTGTCTGTCTAAGAAACAAGAGGAATTTA 3780
3840 Db TCTACTAGGCATAGCAACCTTGTACCGAGTGTCTGTCTAAGAAACAAGAGGAATTTA 3899
3781 QY TTATCACTGAAGATAGCTTAAATGATGCTGACGTAAACAGGTAATAATTGCAAGGATCT 3840
3900 Db TTATCACTGAAGATAGCTTAAATGATGCTGACGTAAACAGGTAATAATTGCAAGGATCT 3959
3841 QY CAGGAACATCACCTTAGTGAGGAAAACAAAATGTTCTGTGCTAGCTGTTTCTTCCAGAGTC 3900
3960 Db CAGGAACATCACCTTAGTGAGGAAAACAAAATGTTCTGTGCTAGCTGTTTCTTCCAGAGTC 4019
3901 QY AGTGAATTTGGAGACTTTGATCTGCAATAAACAACCCAGGATCCTTTCTTGTGTTCT 3960
4020 Db AGTGAATTTGGAGACTTTGATCTGCAATAAACAACCCAGGATCCTTTCTTGTGTTCT 4079
3961 QY TCCAAAACAAATGAGGATCAGTCTGAAAAGCCAGGAGTTGGTCTGAGTGACAGGAATTG 4020
4080 Db TCCAAAACAAATGAGGATCAGTCTGAAAAGCCAGGAGTTGGTCTGAGTGACAGGAATTG 4139
4021 QY GTTTCAGATGATGAAGAAAGAGAAACGGGCTTGGAGAGAAAATTAATCAAGAGAGCAAGC 4080

Db 4140 GTTTCAGATGATGAGAGAGAGAAACGGCTTUGAGAGAAATTAATCAAGAGAGCAAGC 4199
Qy 4081 ATGGATTCAAATTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAACAAAGAGCTCTCTGAA 4140
Db 4200 ATGGATTCAAATTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAACAAAGAGCTCTCTGAA 4259
Qy 4141 GACTGCTCAGGGCTATCCTCTCAGAGTGACATTTAAACCACTCAGCAGAGGGATACCATG 4200
Db 4260 GACTGCTCAGGGCTATCCTCTCAGAGTGACATTTAAACCACTCAGCAGAGGGATACCATG 4319
Qy 4201 CAACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAGCTGTGTAGAACAG 4260
Db 4320 CAACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAGCTGTGTAGAACAG 4379
Qy 4261 CATGGAGAGCCAGCTTTCAACAGCTACCTTCCATCATAAGTGACTCTTCTGCCCCTTGAG 4320
Db 4380 CATGGAGAGCCAGCTTTCAACAGCTACCTTCCATCATAAGTGACTCTTCTGCCCCTTGAG 4439
Qy 4321 GACTCGGAAATCCAGAACAAAGCACAATCAGAAAAAGCAGTATTAACTTCAAGAAAAAGT 4380
Db 4440 GACTCGGAAATCCAGAACAAAGCACAATCAGAAAAAGCAGTATTAACTTCAAGAAAAAGT 4499
Qy 4381 AGTGAATACCTTATAAGCCAGAAATCAGAAAGGCTTTCTGTGACAAAGTTGAGGTGCT 4440
Db 4500 AGTGAATACCTTATAAGCCAGAAATCAGAAAGGCTTTCTGTGACAAAGTTGAGGTGCT 4559
Qy 4441 GCAGATAGTCTACCAAGTAAATAAAGAACACAGGAGTGGAAGTCACTCCCTCTCAA 4500
Db 4560 GCAGATAGTCTACCAAGTAAATAAAGAACACAGGAGTGGAAGTCACTCCCTCTCAA 4619
Qy 4501 TGGCCATCATATGATAGTGGTGCATGCAAGTTGCTCTGGGAGTCTTCAGAAATAGA 4560
Db 4620 TGGCCATCATATGATAGTGGTGCATGCAAGTTGCTCTGGGAGTCTTCAGAAATAGA 4679
Qy 4561 AACTACCCATCTCAAGAGAGCTCATTAAAGTGTGTTGATGTGGAGGAGCAACAGCTGGAA 4620
Db 4680 AACTACCCATCTCAAGAGAGCTCATTAAAGTGTGTTGATGTGGAGGAGCAACAGCTGGAA 4739
Qy 4621 GAGTCTGGGCCACACGATTGACGAAACATCTTACTTCCCAAGGCAAGATCTAGAGGA 4680
Db 4740 GAGTCTGGGCCACACGATTGACGAAACATCTTACTTCCCAAGGCAAGATCTAGAGGA 4799
Qy 4681 ACCCTTACTCTGGATCTGGATCAGCTTCTCTGATGACCCCTGAATCTGATCCTCT 4740
Db 4800 ACCCTTACTCTGGATCTGGATCAGCTTCTCTGATGACCCCTGAATCTGATCCTCT 4859
Qy 4741 GAAGCAGAGCCCCAGAGTCAGTCTGCTGTGGCAACATACCTTCAACCTCTGCTATG 4800
Db 4860 GAAGCAGAGCCCCAGAGTCAGTCTGCTGTGGCAACATACCTTCAACCTCTGCTATG 4919
Qy 4801 AAAGTTCGCCAATTGAAGTTGAGAAATCTGCCAGGGTCCAGCTGCTGCTCATACTACT 4860
Db 4920 AAAGTTCGCCAATTGAAGTTGAGAAATCTGCCAGGGTCCAGCTGCTGCTCATACTACT 4979
Qy 4861 GATACTGCTGGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGGAGCAAGAAATTGACA 4920
Db 4980 GATACTGCTGGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGGAGCAAGAAATTGACA 5039
Qy 4921 GCTTCAACAGAAAGGTTCAACAAAGAAATGTCATGGTGTGCTGGCTGACCCCGAGAA 4980
Db 5040 GCTTCAACAGAAAGGTTCAACAAAGAAATGTCATGGTGTGCTGGCTGACCCCGAGAA 5099
Qy 4981 GAATTTATGCTGCTGTACAGTTTGCAGAAACACCAATCATTCTTAATCTAATTT 5040
Db 5100 GAATTTATGCTGCTGTACAGTTTGCAGAAACACCAATCATTCTTAATCTAATTT 5159
Qy 5041 ACTGAAGAGACTACTCATGCTGTATGAAACAGAGTGTGAGTGTGTGTGAGAGGACA 5100
Db 5160 ACTGAAGAGACTACTCATGCTGTATGAAACAGAGTGTGAGTGTGTGTGAGAGGACA 5219
Qy 5101 CTGAAATATTTCTAGGAATTCGGGAGGAAATGGGTAGTTAGCTATTCTTGGGTGACC 5160

Db 5220 CTGAAATATTTCTAGGAATTCGGGAGGAAATGGGTAGTTAGCTATTCTTGGGTGACC 5279
Qy 5161 CAGTCTATTAAAGAAAGAAATATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGTG 5220
Db 5280 CAGTCTATTAAAGAAAGAAATATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGTG 5339
Qy 5221 GTCAATGGAAGAAACCAACAGGTCCAAAGCGAGCAAGAGAAATCCAGAGACAGAAAGATC 5280
Db 5340 GTCAATGGAAGAAACCAACAGGTCCAAAGCGAGCAAGAGAAATCCAGAGACAGAAAGATC 5399
Qy 5281 TFCAGGGGCTAGAAATCTGTGCTATGGGCCCTTCCAAACATGCCACAGATCAACTG 5340
Db 5400 TFCAGGGGCTAGAAATCTGTGCTATGGGCCCTTCCAAACATGCCACAGATCAACTG 5459
Qy 5341 GAAATGATGCTACAGCTGTGGTCTCTTCTGTGGTGAAGGAGCTTTTCATCTACCCCTT 5400
Db 5460 GAAATGATGCTACAGCTGTGGTCTCTTCTGTGGTGAAGGAGCTTTTCATCTACCCCTT 5519
Qy 5401 GGCACAGGTGTCACCCCAATTTGTGTTGTGACGAGCAGATGCTGACAGAGCAATGAC 5460
Db 5520 GGCACAGGTGTCACCCCAATTTGTGTTGTGACGAGCAGATGCTGACAGAGCAATGAC 5579
Qy 5461 TTCATGCAATTTGGGCAAGATGTGAGGCACTGTGGTGAACCCGAGAGTGGGTGTGGAC 5520
Db 5580 TTCATGCAATTTGGGCAAGATGTGAGGCACTGTGGTGAACCCGAGAGTGGGTGTGGAC 5639
Qy 5521 AGTGTAGCACTCTACAGTGCAGGAGCTGGACACTTACCTGATACCCCGAC 5580
Db 5640 AGTGTAGCACTCTACAGTGCAGGAGCTGGACACTTACCTGATACCCCGAC 5699
Qy 5581 AGCCACTAC 5589
Db 5700 AGCCACTAC 5708

RESULT 15

US-08-986-106-1
; Sequence 1, Application US/08986106
; Patent No. 6177410
; GENERAL INFORMATION:
; APPLICANT: HOLT, JEFFREY T.
; APPLICANT: JENSEN, ROY A.
; APPLICANT: KING, MARY-CLAIRE
; APPLICANT: STEINER, MITCHELL S.
; APPLICANT: ROBINSON-BENION, CHERYL L.
; APPLICANT: THOMPSON, MARILYN E.
; TITLE OF INVENTION: THERAPEUTIC METHODS FOR
; TITLE OF SEQUENCES: 26
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
; COMPUTER: IBM PC/XT/AT compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,106
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/603,753
; FILING DATE: 20 FEB 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ARLES A. TAYLOR, JR.
; REGISTRATION NUMBER: 39,395
; REFERENCE/DOCKET NUMBER: 1242/3

TELECOMMUNICATION INFORMATION:

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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5712
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

FEATURES:

NAME/KEY: BRCA1
LOCATION: GenBank accession no. U14680
PUBLICATION INFORMATION:
AUTHORS: Miki, Y., et. al.
TITLE: A strong candidate gene for the breast and
TITLE: ovarian cancer susceptibility gene BRCA1.
JOURNAL: Science

VOLUME: 266

PAGES: 66-71

DATE: 1994

US-08-986-106-1

Query Match 99.8%; Score 5579.4; DB 3; Length 5712;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 5583; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	1	ATGGATTATCTGCTCTTCGCGTTGAAGAAGTACAAATGTCTAATATGCTATCGAGAA	60
Db	120	ATGGATTATCTGCTCTTCGCGTTGAAGAAGTACAAATGTCTAATATGCTATCGAGAA	179
Qy	61	ATCTTAGAGTGTCCATCTGCTGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGAC	120
Db	180	ATCTTAGAGTGTCCATCTGCTGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGAC	239
Qy	121	CACATATTTGCAATTTTGCAATCTTCTCAACAGAGAAAGGSCCTTCACAG	180
Db	240	CACATATTTGCAATTTTGCAATCTTCTCAACAGAGAAAGGSCCTTCACAG	299
Qy	181	TGCTCTTATCTAGAGATGATATACCAAGAGGAGCCTACAGAAAGTACAGATTTAGT	240
Db	300	TGCTCTTATCTAGAGATGATATACCAAGAGGAGCCTACAGAAAGTACAGATTTAGT	359
Qy	241	CAACTGTGTGAAGAGCTATTGAAAATCATTTGTGCTTTTTCAGCTTGACACAGGTTTGGAG	300
Db	360	CAACTGTGTGAAGAGCTATTGAAAATCATTTGTGCTTTTTCAGCTTGACACAGGTTTGGAG	419
Qy	301	TATCAACAGCTATATTTTGCAAAAGAGGAAATATCTCTCTGACATCTAAGAT	360
Db	420	TATCAACAGCTATATTTTGCAAAAGAGGAAATATCTCTCTGACATCTAAGAT	479
Qy	361	GAAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCTGCAAGAGCTTCTACAGAT	420
Db	480	GAAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCTGCAAGAGCTTCTACAGAT	539
Qy	421	GAACCCGAAATCTCTCTGAGGAAACAGTCTCAGTGTCCAACTCTCTACCTTTGGA	480
Db	540	GAACCCGAAATCTCTCTGAGGAAACAGTCTCAGTGTCCAACTCTCTACCTTTGGA	599
Qy	481	ACTGTGAGAACTCTGAGGACAAAGCAGCGATACAACTCTCAAGAGCTCTGTCTACAT	540
Db	600	ACTGTGAGAACTCTGAGGACAAAGCAGCGATACAACTCTCAAGAGCTCTGTCTACAT	659
Qy	541	GAATTTGGATCTGATCTTCTGAGATACCGTTTAATAGGCAACTTATTCAGTGTGGGA	600
Db	660	GAATTTGGATCTGATCTTCTGAGATACCGTTTAATAGGCAACTTATTCAGTGTGGGA	719
Qy	601	GATCAGAAATTTTACAAATCCCTCAGGACACCGGATGAATCAGTTTGGATCT	660
Db	720	GATCAGAAATTTTACAAATCCCTCAGGACACCGGATGAATCAGTTTGGATCT	779
Qy	661	GCAAAAAGGCTGCTGTGAAATTTTCTGAGACCGATGTAACTAATCTGAAATATCA	720
Db	780	GCAAAAAGGCTGCTGTGAAATTTTCTGAGACCGATGTAACTAATCTGAAATATCA	839

Qy	721	CCAGTAATAATGATTGTAACCACTGAGAGCGTGCAGCTGAGAGGATCCAGAAAG	780
Db	840	CCAGTAATAATGATTGTAACCACTGAGAGCGTGCAGCTGAGAGGATCCAGAAAG	899
Qy	781	TATCAGGAGTGTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCAAAATATCTATGCC	840
Db	900	TATCAGGAGTGTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCAAAATATCTATGCC	959
Qy	841	AGCTCATATACAGCATGAGACACGCGTTTATTAATCTCACTAAAGACAGATGATGTAGAA	900
Db	960	AGCTCATATACAGCATGAGACACGCGTTTATTAATCTCACTAAAGACAGATGATGTAGAA	1019
Qy	901	AAGGCTGAATTTCTGTAATTAAGCAAAACAGCTTGGCTTAGCAAGGAGCCAACTAACA	960
Db	1020	AAGGCTGAATTTCTGTAATTAAGCAAAACAGCTTGGCTTAGCAAGGAGCCAACTAACA	1079
Qy	961	TGGGCTGGAAGTAAGGAAACATGTATATGATGGCGGACTCCAGGACAGAAAAAGGTA	1020
Db	1080	TGGGCTGGAAGTAAGGAAACATGTATATGATGGCGGACTCCAGGACAGAAAAAGGTA	1139
Qy	1021	GATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGCAATTAAGCAGAAACTGCCATGC	1080
Db	1140	GATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGCAATTAAGCAGAAACTGCCATGC	1199
Qy	1081	TCAGAGAAATCTTAGAGATCTGAAGATGTTCTTGTGATTAACATAATAGCAGCATTCAG	1140
Db	1200	TCAGAGAAATCTTAGAGATCTGAAGATGTTCTTGTGATTAACATAATAGCAGCATTCAG	1259
Qy	1141	AAAGTTAAATGAGTGGTTCCTCAAGAGTGAATGTTAGTGGTTCATGATCACTACATGAT	1200
Db	1260	AAAGTTAAATGAGTGGTTCCTCAAGAGTGAATGTTAGTGGTTCATGATCACTACATGAT	1319
Qy	1201	GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTAATGGAAGCTTCTAAATAGGTAGAT	1260
Db	1320	GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTAATGGAAGCTTCTAAATAGGTAGAT	1379
Qy	1261	GATATTTCTGTTCTTTCAGAGAAATAGACTTCTGCGCAGTGTCTCATGAGGCTTTA	1320
Db	1380	GATATTTCTGTTCTTTCAGAGAAATAGACTTCTGCGCAGTGTCTCATGAGGCTTTA	1439
Qy	1321	ATATGTAAGAGTGAAGAGTTCTCACTCAAAATCAGTAGAGAGTAATATTGAAGACAAATA	1380
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Qy	1381	TTTGGGAAACCTTATCGGAGAGGCAAGCCTCCCACTTAAGCCATGTACTGTAAT	1440
Db	1500	TTTGGGAAACCTTATCGGAGAGGCAAGCCTCCCACTTAAGCCATGTACTGTAAT	1559
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Job time : 34s secs

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CM nucleic - nucleic search, using sw model

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Title: US-09-734-672a-3_COPY_120_5708

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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	5589	100.0	5711	6	AR112809	AR112809 Sequence
3	5587.4	100.0	5711	6	AR007333	AR007333 Sequence
4	5587.4	100.0	5711	6	AR112808	AR112808 Sequence
5	5587.4	100.0	5711	6	IS9546	Sequence 1
6	5581	99.9	5711	6	AR007334	AR007334 Sequence
7	5581	99.9	5711	6	AR112810	AR112810 Sequence
8	5579.4	99.8	5711	6	AR033056	AR033056 Sequence
9	5579.4	99.8	5711	6	AX659576	AX659576 Sequence
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13	5579.4	99.8	5712	6	AR125601	AR125601 Sequence
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41	5565.4	99.6	5709	6	I40800	Sequence 9
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44	5565.4	99.6	5709	6	AR278116	AR278116 Sequence
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ALIGNMENTS

RESULT 1	AR007335	Sequence 5 from patent US 5750400.	5711 bp	DNA	linear	PAT 04-DEC-1998
LOCUS	AR007335	Sequence 5 from patent US 5750400.	5711 bp	DNA	linear	PAT 04-DEC-1998
DEFINITION	AR007335	Sequence 5 from patent US 5750400.	5711 bp	DNA	linear	PAT 04-DEC-1998
ACCESSION	AR007335	Sequence 5 from patent US 5750400.	5711 bp	DNA	linear	PAT 04-DEC-1998
VERSION	AR007335.1	GI:3966819	5711 bp	DNA	linear	PAT 04-DEC-1998
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 5711)					
AUTHORS	Murphy,P.D., Allen,A.C., Alvares,C.P., Critz,B.S., Olson,S.J., Schelter,D.B. and Zeng,B.					
TITLE	Coding sequences of the human BRCA1 gene					
JOURNAL	Patent: US 5750400-A 5 12-MAY-1998;					

FEATURES		Location/Qualifiers	
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		/organism="unknown"	
		/mol_type="unassigned DNA"	
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	Best Local Similarity	100.0%; Pred. No. 0;	
	Matches 5589; Conservative	0; Mismatches	0; Gaps
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DB	120	ATGGAATTATCTGCTTTCGGGTTGGAAGATGACAAATGTCTTAATGCTATGCGAAA	179
QY	61	ATCTTAGAGTCCCATCTGCTGAGTGTGATGAGGAACTGTCTCCCAAAAGTGTGAC	120
DB	180	ATCTTAGAGTGTCCCATCTGCTGAGTGTGATGAGGAACTGTCTCCCAAAAGTGTGAC	239
QY	121	CACATATTTTCCAAATTTTGATGCTGCTCAACAGGAAAGAGGCGCTTTCACAG	180
DB	240	CACATATTTTCCAAATTTTGATGCTGCTCAACAGGAAAGAGGCGCTTTCACAG	299
QY	181	TGTCCTTTATGATGATGATATACCAAGGAGGCTTACAGAAAGTACAGATTTAGT	240
DB	300	TGTCCTTTATGATGATGATATACCAAGGAGGCTTACAGAAAGTACAGATTTAGT	359
QY	241	CAACTTGTGAGAGCTATTGAAATCATTTGTGCTTTTCAAGCTTGACACAGGTTTGGAG	300
DB	360	CAACTTGTGAGAGCTATTGAAATCATTTGTGCTTTTCAAGCTTGACACAGGTTTGGAG	419
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DB	420	TATGCAAAACAGCTATAATTTTGAAGAAAGGAAATTAATCTCTCGAACAATCTAAAGAT	479
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1500	TTTGGGAAACCTATTCGGAAGAGCGCTCCCAACTTTAAGCCATGTAACTGAAAAAT	1559
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LOCUS			
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ACCESSION ARL12809			
VERSION ARL12809.1 GI:14092709			
KEYWORDS			
SOURCE Unknown.			
ORGANISM Unclassified.			
REFERENCE			
AUTHORS Murphy, P.D., Allen, A.C.P., Alvares, C.P., Critz, B.S., Olson, S.J., Thurber, D. and Zeng, B.			
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Db	180	ATCTTAGAGTGTCCTCTCTCTCTGAGTTGATCAAGAACCTGCTCTCCAAAGTGTGAC	239
Qy	121	CACATATTTTGCAAAATTTTGCATCTCTGAAACTTCTCAACCAAGAAAGGGCCTTCAAG	180
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Qy 2281 GAAAGATCTGTAGAGAGTAGCAGATTTTCACTGGTACCTGGTACTGATTTATGGCACTCAG 2340
Db 2400 GAAAGATCTGTAGAGAGTAGCAGATTTTCACTGGTACCTGGTACTGATTTATGGCACTCAG 2459
Qy 2341 GAAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAACCAATATAA 2400
Db 2460 GAAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAACCAATATAA 2519
Qy 2401 FGTGTGAGTCACTGTGCAGCATTTGAAAAACCCCAAGGGAAGTAAATTCATGGTTGTTCCAAA 2460
Db 2520 TGTGTGAGTCACTGTGCAGCATTTGAAAAACCCCAAGGGAAGTAAATTCATGGTTGTTCCAAA 2579
Qy 2461 GATAATAGAAATGACACAGAGGCTTTTAAAGTATCAATTTGGGACATGAACTTAACCACT 2520
Db 2580 GATAATAGAAATGACACAGAGGCTTTTAAAGTATCAATTTGGGACATGAACTTAACCACT 2639
Qy 2521 CCGGAAAACAAGCATAGAAATGGAAGTGAAGTAACTTTGATGCTCAGTATTTGAGAAATACA 2580
Db 2640 CCGGAAAACAAGCATAGAAATGGAAGTGAAGTAACTTTGATGCTCAGTATTTGAGAAATACA 2699
Qy 2581 TTCAAAGTTTCAAAGCGCCAGTCATTTGCTCTGTTTTCAAATCCAGGAAATCCGAGAGAG 2640
Db 2700 TTCAAAGTTTCAAAGCGCCAGTCATTTGCTCTGTTTTCAAATCCAGGAAATCCGAGAGAG 2759
Qy 2641 GAATGTGCAACATCTCTGCCCACTCTGGCTCTTAAAGAAACAAAGTCCAAAAGTCACT 2700
Db 2760 GAATGTGCAACATCTCTGCCCACTCTGGCTCTTAAAGAAACAAAGTCCAAAAGTCACT 2819
Qy 2701 TTTGAAATGTGAACAAAAGGAGAAAATCAAGGAAAGAAATGAGTCTAATATCAAGGCTGTA 2760
Db 2820 TTTGAAATGTGAACAAAAGGAGAAAATCAAGGAAAGAAATGAGTCTAATATCAAGGCTGTA 2879
Qy 2761 CAGACAGTTAATATCACTGCGAGGCTTCTGTTGGTGCAGAAAGATAAGCCAGTTGAT 2820
Db 2880 CAGACAGTTAATATCACTGCGAGGCTTCTGTTGGTGCAGAAAGATAAGCCAGTTGAT 2939
Qy 2821 AATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTTGCTATCATCTCAGTTCCAGAGGC 2880
Db 2940 AATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTTGCTATCATCTCAGTTCCAGAGGC 2999
Qy 2881 AACGAAAATGGAATCAATTAATCAATTAATCAATTAATCAATTAATCAATTAATCAATTAAT 2940
Db 3000 AACGAAAATGGAATCAATTAATCAATTAATCAATTAATCAATTAATCAATTAATCAATTAAT 3059
Qy 2941 CCACCACTTTTTTCCCACTCAAGTCAATTTGTTAAAACTAAATGTAAAGAAAATCTGCTAGAG 3000
Db 3060 CCACCACTTTTTTCCCACTCAAGTCAATTTGTTAAAACTAAATGTAAAGAAAATCTGCTAGAG 3119
Qy 3001 GAAAACTTTGAGGAACTTCAATGTCACTGAAAGAGAAAATGGGAAATGAGAACTTCCA 3060
Db 3120 GAAAACTTTGAGGAACTTCAATGTCACTGAAAGAGAAAATGGGAAATGAGAACTTCCA 3179
Qy 3061 AGTACAGTACAGCACTTAGCCGTAAATTAACATTAAGAGAAAATGTTTTTAAAGAGGACGAG 3120
Db 3180 AGTACAGTACAGCACTTAGCCGTAAATTAACATTAAGAGAAAATGTTTTTAAAGAGGACGAG 3239

QY 3121 TCAGCAATTAATGAAGTAGGTTCCAGTACTAATCAAGTGGCTCCAGTATTAATGAA 3180
DB 3240 TCAGCAATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGCTCCAGTATTAATGAA 3299
QY 3181 ATAGGTTCCAGTATGAAGTAAATCAATTCAGAGAGAACTAGTAGAGAAACAGAGGGGCCAAATTTG 3240
DB 3300 ATAGGTTCCAGTATGAAGTAAATCAATTCAGAGAGAACTAGTAGAGAAACAGAGGGGCCAAATTTG 3359
QY 3241 AATGCTATGCTTAGGTTAGGGTTTTCACCTGAGGCTCTATAACAAAGTCTTCCTGGA 3300
DB 3360 AATGCTATGCTTAGGTTAGGGTTTTCACCTGAGGCTCTATAACAAAGTCTTCCTGGA 3419
QY 3301 AGTAAATTTGAAGTATCTGAAATTAATAAAGCAAGATATGAAGAGTAGTTTCAGACTGTT 3360
DB 3420 AGTAAATTTGAAGTATCTGAAATTAATAAAGCAAGATATGAAGAGTAGTTTCAGACTGTT 3479
QY 3361 AATACAGATTTCTCTCCATATCTGATTTTCAGATTAACCTTAGAGACAGCTATGGGAAGTAGT 3420
DB 3480 AATACAGATTTCTCTCCATATCTGATTTTCAGATTAACCTTAGAGACAGCTATGGGAAGTAGT 3539
QY 3421 CATGCATCTCAGGTTTCTCTGAGACACCTGATGACCTGTTAGATGATGCTGAAATAAAG 3480
DB 3540 CATGCATCTCAGGTTTCTCTGAGACACCTGATGACCTGTTAGATGATGCTGAAATAAAG 3599
QY 3481 GAAGATACTAGTTTCTGAAAAATGACATTAAGGAAAGTTCTGCTGTTTTTAGCAAAAGC 3540
DB 3600 GAAGATACTAGTTTCTGAAAAATGACATTAAGGAAAGTTCTGCTGTTTTTAGCAAAAGC 3659
QY 3541 GTCCAGAGAGAGCTTACAGAGAGCTTAGGCTTACCCATACACATATGGCTCAG 3600
DB 3660 GTCCAGAGAGAGCTTACAGAGAGCTTAGGCTTACCCATACACATATGGCTCAG 3719
QY 3601 GGTTCACGAGAGGGGCCAAGAAATAGAGTCTCTCAGAGAGAACTTATCTAGTGAGGAT 3660
DB 3720 GGTTCACGAGAGGGGCCAAGAAATAGAGTCTCTCAGAGAGAACTTATCTAGTGAGGAT 3779
QY 3661 GAAGAGCTTCCCTGCTCCAACTCTGTTATTTGGTAAAGTAAACATATACCTTCTCAG 3720
DB 3780 GAAGAGCTTCCCTGCTCCAACTCTGTTATTTGGTAAAGTAAACATATACCTTCTCAG 3839
QY 3721 TCTACTAGGATAGCAGCTGCTTACCGAGTGTCTGTCTAGAGACACAGAGAGAGATTTA 3780
DB 3840 TCTACTAGGATAGCAGCTGCTTACCGAGTGTCTGTCTAGAGACACAGAGAGAGATTTA 3899
QY 3781 TTATCATTTGAAGATAGCTTAATFAGTCTCAGTAAACAGATATATTTGGCAAGGCACTCT 3840
DB 3900 TTATCATTTGAAGATAGCTTAATFAGTCTCAGTAAACAGATATATTTGGCAAGGCACTCT 3959
QY 3841 CAGGACATCACCTTAGTGAGGAAACAAATGTTCTGCTAGTGTGTTTCTTCCAGAGTGC 3900
DB 3960 CAGGACATCACCTTAGTGAGGAAACAAATGTTCTGCTAGTGTGTTTCTTCCAGAGTGC 4019
QY 3901 AGTGAATTTGAAGACTTTGACTGCAAAATACAAACACCCAGGATCCTTTCTTTGATTTGTTCT 3960
DB 4020 AGTGAATTTGAAGACTTTGACTGCAAAATACAAACACCCAGGATCCTTTCTTTGATTTGTTCT 4079
QY 3961 TCCAAACAAATGAGGATCTAGTCTGAAAGCAGGAGTTGGTCTGAGTGAACAGGATTTG 4020
DB 4080 TCCAAACAAATGAGGATCTAGTCTGAAAGCAGGAGTTGGTCTGAGTGAACAGGATTTG 4139
QY 4021 GTTTTCAGATGATGAAGAAAGAGGAAACCGGCTTGGAGAAATTAATCAAGAGAGCAAGAGC 4080
DB 4140 GTTTTCAGATGATGAAGAAAGAGGAAACCGGCTTGGAGAAATTAATCAAGAGAGCAAGAGC 4199
QY 4081 ATGGATTTCAAATTTAGTGAAGCAGCATCTGGGTGTGAGAGTGAACAAAGCGTCTCTGAA 4140
DB 4200 ATGGATTTCAAATTTAGTGAAGCAGCATCTGGGTGTGAGAGTGAACAAAGCGTCTCTGAA 4259
QY 4141 GACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAACTCTCAGAGAGGATACCATG 4200
DB 4260 GACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAACTCTCAGAGAGGATACCATG 4319
QY 4201 CAACATAACCTGATAAAGCTCCAGAGGAAATGGCTGAACCTAGAGCTGTGTTAGAACAG 4260

DB 4320 CAACTAATCTGATTAAGCTCCAGCGGAATGGCTGAACCTAGAGCTGTGTTAGAACAG 4379
QY 4261 CATGGAGCCAGCTTTCTAACAGCTACCCCTTCCATCATTAAGTGACCTTTCTGCCCCTTGAG 4320
DB 4380 CATGGAGCCAGCTTTCTAACAGCTACCCCTTCCATCATTAAGTGACCTTTCTGCCCCTTGAG 4439
QY 4321 GACCTGCGAAATCCAGAACAAAGCAATCAGAAAAAGCAGTATTAACTTTACAGAAAAAGT 4380
DB 4440 GACCTGCGAAATCCAGAACAAAGCAATCAGAAAAAGCAGTATTAACTTTACAGAAAAAGT 4499
QY 4381 AGTGAATACCTTATAAGCCAGAAATCCAGAGGCCCTTTCTGCTGACAAAGTTTGAGGTGCT 4440
DB 4500 AGTGAATACCTTATAAGCCAGAAATCCAGAGGCCCTTTCTGCTGACAAAGTTTGAGGTGCT 4559
QY 4441 GCAGATAGTTCTACCAAGTAAAAATAAGAACACAGAGTGAAGGTCACTCCCTTCTTAA 4500
DB 4560 GCAGATAGTTCTACCAAGTAAAAATAAGAACACAGAGTGAAGGTCACTCCCTTCTTAA 4619
QY 4501 TGCCTCATCATTAAGATGATAGTGGTACATGCACAGTTGCTCTGGAGTCTTTCAGAAATAGA 4560
DB 4620 TGCCTCATCATTAAGATGATAGTGGTACATGCACAGTTGCTCTGGAGTCTTTCAGAAATAGA 4679
QY 4561 AACTACCCATCTCAGAGAGGCTCAATTAAGTTTGTGATGTGGAGAGCAACGCTGGAA 4620
DB 4680 AACTACCCATCTCAGAGAGGCTCAATTAAGTTTGTGATGTGGAGAGCAACGCTGGAA 4739
QY 4621 GAGTCTGGCCACACAGATTTGAGGAAACATCTTCTGCCAAGGCAAGATCTAGAGGGA 4680
DB 4740 GAGTCTGGCCACACAGATTTGAGGAAACATCTTCTGCCAAGGCAAGATCTAGAGGGA 4799
QY 4681 ACCCTTACTTGGAAATCTGGAATFAGCCCTTCTCTGATGACCCCTGAATCTGATCTTCT 4740
DB 4800 ACCCTTACTTGGAAATCTGGAATFAGCCCTTCTCTGATGACCCCTGAATCTGATCTTCT 4859
QY 4741 GAAGCAGAGCCCGAGAGTCACTGCTTGGCAACATACCATCTTCACTCTCTCATG 4800
DB 4860 GAAGCAGAGCCCGAGAGTCACTGCTTGGCAACATACCATCTTCACTCTCTCATG 4919
QY 4801 AAAGTTTCCCAATTTGAAGTTGACAGATCTGCCAGGGTCCAGCTCTCATACTACT 4860
DB 4920 AAAGTTTCCCAATTTGAAGTTGACAGATCTGCCAGGGTCCAGCTCTCATACTACT 4979
QY 4861 GATCTGCTGGGTATTAATGCAATGGAAGAGTGTGAGGAGGAGAGGAGCAAGATGACA 4920
DB 4980 GATCTGCTGGGTATTAATGCAATGGAAGAGTGTGAGGAGGAGAGGAGCAAGATGACA 5039
QY 4921 GCTTCAACAGAAAGGCTCAACAAAGATGCTCATGTTGGTGTCTGGCTTGAACCCAGAA 4980
DB 5040 GCTTCAACAGAAAGGCTCAACAAAGATGCTCATGTTGGTGTCTGGCTTGAACCCAGAA 5099
QY 4981 GAATTTATGCTCTGTTACAAAGTTTGCAGAAACACCATCATCTTTAACTTAATCTAAT 5040
DB 5100 GAATTTATGCTCTGTTACAAAGTTTGCAGAAACACCATCATCTTTAACTTAATCTAAT 5159
QY 5041 ACTGAGAGACTACTCATGCTGTATGAACAGAGTGTGAGTGTGTTGTGTCACGACA 5100
DB 5160 ACTGAGAGACTACTCATGCTGTATGAACAGAGTGTGAGTGTGTTGTGTCACGACA 5219
QY 5101 CTGAAATATTTCTAGGAATTCGCGAGGAAATCGGTAGTTAGCTATTTCTGGGTGACC 5160
DB 5220 CTGAAATATTTCTAGGAATTCGCGAGGAAATCGGTAGTTAGCTATTTCTGGGTGACC 5279
QY 5161 CAGTCTTATTAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGATGAG 5220
DB 5280 CAGTCTTATTAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGATGAG 5339
QY 5221 GTCAATGGAAGAAACCAACAGCTCCAAAGCGAGCAAGAGATCCAGAGCAAGAAATC 5280
DB 5340 GTCAATGGAAGAAACCAACAGCTCCAAAGCGAGCAAGAGATCCAGAGCAAGAAATC 5399
QY 5281 TTCAGGGGCTAGAAATCTGTTGCTATGCGCCCTTCAACACATGCCCCACAGATCAACTG 5340

Db 1560 CTAATTATAGGAGCAATTTGTACTAGGCCACAGATAAATACAGAGCGCTCCCTCCACAAT 1619
Qy 1501 AAATTTAAAGCGTAAAGGAGACCTACATCAGCGCTTTATCTCTGAGATTTTATCAAGAAA 1560
Db 1620 AAATTTAAAGCGTAAAGGAGACCTACATCAGCGCTTTATCTCTGAGATTTTATCAAGAAA 1679
Qy 1561 GCAGATTTGGCAGTTCAAAAGACTCTCTGAATGATAAATCAGGGAACTAAACAAACGGAG 1620
Db 1680 GCAGATTTGGCAGTTCAAAAGACTCTCTGAATGATAAATCAGGGAACTAAACAAACGGAG 1739
Qy 1621 CAGAAATGCTCAAGTGAATGATTAATTAATAGTGGTCAATGAGATAAATAAAGAGGTGAT 1680
Db 1740 CAGAAATGCTCAAGTGAATGATTAATTAATAGTGGTCAATGAGATAAATAAAGAGGTGAT 1739
Qy 1681 TCTATTCCAGATAGAGAAAATCTTAACCCCAATAGAACTCACTCGAAAAAGAACTGCTTTTC 1740
Db 1800 TCTATTCCAGATAGAGAAAATCTTAACCCCAATAGAACTCACTCGAAAAAGAACTGCTTTTC 1859
Qy 1741 AAAACGAAAGCTGAACCTTATAGCAGCAGTATAGCAATATAGCAATATGGAACCTCGAATTAATATC 1800
Db 1860 AAAACGAAAGCTGAACCTTATAGCAGCAGTATAGCAATATGGAACCTCGAATTAATATC 1919
Qy 1801 CACAATTCAAAAGCACTTAAAGAAATAGGCTGAGGAGAACTCTTTTACAGGCAATTT 1860
Db 1920 CACAATTCAAAAGCACTTAAAGAAATAGGCTGAGGAGAACTCTTTTACAGGCAATTT 1979
Qy 1861 CATGGCTTGAACTAGTACTAGTGAATCTTAAGCCCACTTAATGTTACTGAATTCGAA 1920
Db 1980 CATGGCTTGAACTAGTACTAGTGAATCTTAAGCCCACTTAATGTTACTGAATTCGAA 2039
Qy 1921 ATTGATAGTCTTTCTAGCAGTGAAGAGATAAAGAAAAAAGTCAACCAATCCCAATC 1980
Db 2040 ATTGATAGTCTTTCTAGCAGTGAAGAGATAAAGAAAAAAGTCAACCAATCCCAATC 2099
Qy 1981 AGGCACAGCAGAACTTACACTCATGGAAGTTAAAGAACTTGCACCTGAGGCCAAAGAG 2040
Db 2100 AGGCACAGCAGAACTTACACTCATGGAAGTTAAAGAACTTGCACCTGAGGCCAAAGAG 2159
Qy 2041 AGTAAACAGCCAAATGAACAGCAAGTAAAGACATGACAGTGAATCTTTCCACAGAGCTG 2100
Db 2160 AGTAAACAGCCAAATGAACAGCAAGTAAAGACATGACAGTGAATCTTTCCACAGAGCTG 2219
Qy 2101 AAGTTAAACAAATGCACTGGTCTTTTACTAAGTTGTTCAATACCACTGAATCTTAAAGAA 2160
Db 2220 AAGTTAAACAAATGCACTGGTCTTTTACTAAGTTGTTCAATACCACTGAATCTTAAAGAA 2279
Qy 2161 TTTGTCATCTAGCTTCCAGAGAGCAAAAGAGCAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2220
Db 2280 TTTGTCATCTAGCTTCCAGAGAGCAAAAGAGCAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2339
Qy 2221 TCTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTTCGAAACT 2280
Db 2340 TCTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTTCGAAACT 2399
Qy 2281 GAAGATCTGTAGAGAGTACGAGTATTTCACTGGTACTGGTACTGATTAATGACACTCAG 2340
Db 2400 GAAGATCTGTAGAGAGTACGAGTATTTCACTGGTACTGGTACTGATTAATGACACTCAG 2459
Qy 2341 GAAAGTATCTGGTACTGGAGTTAGCACTCTAGGGAAGCAAAACAGAACCAATATAA 2400
Db 2460 GAAAGTATCTGGTACTGGAGTTAGCACTCTAGGGAAGCAAAACAGAACCAATATAA 2519
Qy 2401 TGTGTGAGTGTGTGAGCAAGTTTGAAGTATCCATTGGGACATGAAGTTAAACCAAGT 2460
Db 2520 TGTGTGAGTGTGTGAGCAAGTTTGAAGTATCCATTGGGACATGAAGTTAAACCAAGT 2579
Qy 2461 GATAATGAAGTACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAAACCAAGT 2520
Db 2580 GATAATGAAGTACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAAACCAAGT 2639
Qy 2521 CGGAAAACAGCATAGAAAATGGAAGAAAGTGAACCTTGATCTCAGTATTTGCAAGATACA 2580
Db 2640 CGGAAAACAGCATAGAAAATGGAAGAAAGTGAACCTTGATCTCAGTATTTGCAAGATACA 2699

Qy 2581 TTCAAGGTTTCAAGGCCAGTCAATTTGCTCTGTTTTCAATCCAGGAAATGCAGAAGAG 2640
Db 2700 TTCAAGGTTTCAAGGCCAGTCAATTTGCTCTGTTTTCAATCCAGGAAATGCAGAAGAG 2759
Qy 2641 GAATGTCACATTTCTCTGCCACTCTGGGCTCTTAAAGAAACAAAGTCCAAAAGTCACT 2700
Db 2760 GAATGTCACATTTCTCTGCCACTCTGGGCTCTTAAAGAAACAAAGTCCAAAAGTCACT 2819
Qy 2701 TTTGAATGTGAACAAAAGGAGAAATCAAGGAAAGAAATGAGTCTAATATCAAGCTGTGA 2760
Db 2820 TTTGAATGTGAACAAAAGGAGAAATCAAGGAAAGAAATGAGTCTAATATCAAGCTGTGA 2879
Qy 2761 CAGACAGTTAATATCACTGCAAGGCTTCTGCTGGTGGTCCAGAAAGATAAGACCAAGTTGAT 2820
Db 2880 CAGACAGTTAATATCACTGCAAGGCTTCTGCTGGTGGTCCAGAAAGATAAGACCAAGTTGAT 2939
Qy 2821 AATGCCAAATGTAGTATCAAGGAGGCTCTAGGTTTGTCTATCTCTCAAGTCCAGAGGC 2880
Db 2940 AATGCCAAATGTAGTATCAAGGAGGCTCTAGGTTTGTCTATCTCTCAAGTCCAGAGGC 2999
Qy 2881 AACGAAACGTGACTCAATTTACTCCAAATAAACATGGAACCTTTTACAAAACCCATATGATATA 2940
Db 3000 AACGAAACGTGACTCAATTTACTCCAAATAAACATGGAACCTTTTACAAAACCCATATGATATA 3059
Qy 2941 CCACCACTTTTCCCATCAAGTCAATTTGTTTAAACTTAAATGTAAGAAATCTGCTAGAG 3000
Db 3060 CCACCACTTTTCCCATCAAGTCAATTTGTTTAAACTTAAATGTAAGAAATCTGCTAGAG 3119
Qy 3001 GAAAACTTTGAGGAAACATTCATGTCCTCACTGAAAGAAATGGAATGGAATGGAACATTTCCA 3060
Db 3120 GAAAACTTTGAGGAAACATTCATGTCCTCACTGAAAGAAATGGAATGGAATGGAACATTTCCA 3179
Qy 3061 AGTACAGTGAAGCAATTTAGCCTTAATACATTTAGAGAAATGTTTTTAAAGGAGCCAGC 3120
Db 3180 AGTACAGTGAAGCAATTTAGCCTTAATACATTTAGAGAAATGTTTTTAAAGGAGCCAGC 3239
Qy 3121 TCAAGCAATTAATTAAGAGTGGTCCAGTACTTAATGAAGTGGCTCCAGTATTAATGAA 3180
Db 3240 TCAAGCAATTAATTAAGAGTGGTCCAGTACTTAATGAAGTGGCTCCAGTATTAATGAA 3299
Qy 3181 ATAGGTTCCAGTGAATGAAACATTCAGCAGAACCTAGGTAGAAACAGAGGCGCAAAATTTG 3240
Db 3300 ATAGGTTCCAGTGAATGAAACATTCAGCAGAACCTAGGTAGAAACAGAGGCGCAAAATTTG 3359
Qy 3241 AATGCTATCTGATAGTTAGGGTTTTGCAACCTGAGGCTCTATTAACAAAGTCTTCTCTGGA 3300
Db 3360 AATGCTATCTGATAGTTAGGGTTTTGCAACCTGAGGCTCTATTAACAAAGTCTTCTCTGGA 3419
Qy 3301 AGTAAATTTGAAGCATCTTGAATTAAGAAAGCAAGAAATATGAAGAGTGTTCAGACTGTT 3360
Db 3420 AGTAAATTTGAAGCATCTTGAATTAAGAAAGCAAGAAATATGAAGAGTGTTCAGACTGTT 3479
Qy 3361 AATACAGATTTCTTCCATATCTGATTTCCAGATTAATGAAACAGCCTATGGAAGTGT 3420
Db 3480 AATACAGATTTCTTCCATATCTGATTTCCAGATTAATGAAACAGCCTATGGAAGTGT 3539
Qy 3421 CATGCACTCTCAGGTTTGTCTCAGACACCTGATGACCTGTTAGATGATGATGATGATGATGAT 3480
Db 3540 CATGCACTCTCAGGTTTGTCTCAGACACCTGATGACCTGTTAGATGATGATGATGATGATGAT 3599
Qy 3481 GAAGATCTAGTTTGTCTGAAAATGACATTAAGAAAGTCTGCTGTTTTTGTAGCAAAAGC 3540
Db 3600 GAAGATCTAGTTTGTCTGAAAATGACATTAAGAAAGTCTGCTGTTTTTGTAGCAAAAGC 3659
Qy 3541 GTCCAGAGAGGAGAGCTTTAGCAGGAGTCTTACCCCTTTTCCACCATACACATTTGGCTCAG 3600
Db 3660 GTCCAGAGAGGAGAGCTTTAGCAGGAGTCTTACCCCTTTTCCACCATACACATTTGGCTCAG 3719
Qy 3601 GGTATCCGAGAGGAGGCTTAAAGAAATTTAGAGTCTCTCAGAAAGAACTTTATCTAGTGGAGT 3660
Db 3720 GGTATCCGAGAGGAGGCTTAAAGAAATTTAGAGTCTCTCAGAAAGAACTTTATCTAGTGGAGT 3779

QY		3661	GAAGAGCTTCCCTGCTTCCTGCATCAACACTCTGTATTTCGGTAAAGTAACAATAATACCTTTCTCAG	3720
DB		3780	GAAGAGCTTCCCTGCTTCCTGCATCAACACTCTGTATTTCGGTAAAGTAACAATAATACCTTTCTCAG	3839
QY		3721	TCTACTAGGCATAGCACCGTTTGCTACCAGAGTGCTGTGTTCTAAGAACACAGAGGAGCAATTTTA	3780
DB		3840	TCTACTAGGCATAGCACCGTTTGCTACCAGAGTGCTGTGTTCTAAGAACACAGAGGAGCAATTTTA	3899
QY		3781	TTATCATTTGAAGAATAGACTTTAAATGACTGCGAGTAACCAAGGPAATATTGGCAAAGGCATCT	3840
DB		3900	TTATCATTTGAAGAATAGACTTTAAATGACTGCGAGTAACCAAGGPAATATTGGCAAAGGCATCT	3959
QY		3841	CAGGAACATCACCTTAGTGGAGAACAAAATGTTCTGCTAGCTTGTTTTCTTFCACAGTGC	3900
DB		3960	CAGGAACATCACCTTAGTGGAGAACAAAATGTTCTGCTAGCTTGTTTTCTTFCACAGTGC	4019
QY		3901	AGTGAANTGGAGAATTGACTGCGAAATPACAAACACCCAGGATCCTTTCTTGATTTGGTTCT	3960
DB		4020	AGTGAANTGGAGAATTGACTGCGAAATPACAAACACCCAGGATCCTTTCTTGATTTGGTTCT	4079
QY		3961	TCCAAACAAATAGGCCATCAGTCTGAAAGCCAGGGAGTTGCTCTGAGTGCACAGGAATG	4020
DB		4080	TCCAAACAAATAGGCCATCAGTCTGAAAGCCAGGGAGTTGCTCTGAGTGCACAGGAATG	4139
QY		4021	GTTTTCAGATCATGAAGAAGAGGAAACGGGCTTGGAAAGAAAATAATCAAGAAGAGCAAAAGC	4080
DB		4140	GTTTTCAGATCATGAAGAAGAGGAAACGGGCTTGGAAAGAAAATAATCAAGAAGAGCAAAAGC	4199
QY		4081	ATGGAATTTAAACTTAGTGGAGCAGCATCTGGGTGTGAGTGTGAAACAAGCGTCTCTGAA	4140
DB		4200	ATGGAATTTAAACTTAGTGGAGCAGCATCTGGGTGTGAGTGTGAAACAAGCGTCTCTGAA	4259
QY		4141	GACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGGATACCATG	4200
DB		4260	GACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGGATACCATG	4319
QY		4201	CAACATAACCTGTAPAAAGCTCCAGCAGGAAATGCTGAACTAGAGAGCTGTGTAGAACAG	4260
DB		4320	CAACATAACCTGTAPAAAGCTCCAGCAGGAAATGCTGAACTAGAGAGCTGTGTAGAACAG	4379
QY		4261	CATGGGAGCCAGCCTTCTACAGCTACCCCTTCCAATCAATAGTGTACTCTTTGTGCCCTTGAG	4320
DB		4380	CATGGGAGCCAGCCTTCTACAGCTACCCCTTCCAATCAATAGTGTACTCTTTGTGCCCTTGAG	4439
QY		4321	GACCTGCGMAATCCAGAAACCAAGCACATCAGAAAAAGCAGTATTAACTTTCACAGAAAAGT	4380
DB		4440	GACCTGCGMAATCCAGAAACCAAGCACATCAGAAAAAGCAGTATTAACTTTCACAGAAAAGT	4499
QY		4381	AGTGAATACCTTATAAGCCAGAAATCCAGAGGCCCTTTCTGCTGACAGTTTGGAGTGCTCT	4440
DB		4500	AGTGAATACCTTATAAGCCAGAAATCCAGAGGCCCTTTCTGCTGACAGTTTGGAGTGCTCT	4559
QY		4441	GCAGATAGTTCTACAGTAAAMATAAAGAACCCAGGAGTGGAAAGGTCATCCCCCTCTTAAA	4500
DB		4560	GCAGATAGTTCTACAGTAAAMATAAAGAACCCAGGAGTGGAAAGGTCATCCCCCTCTTAAA	4619
QY		4501	TGCCCATCATTAGATAGATAGGTGTATCATGCAAGTTGCTCTGGAGTCTTTCAGAAATAGA	4560
DB		4620	TGCCCATCATTAGATAGATAGGTGTATCATGCAAGTTGCTCTGGAGTCTTTCAGAAATAGA	4679
QY		4561	AACCTACCCATCTCAAGAGGAGCTCATTTAAGTTGCTGATGTGAGGAGGACCAAGCTGGAA	4620
DB		4680	AACCTACCCATCTCAAGAGGAGCTCATTTAAGTTGCTGATGTGAGGAGGACCAAGCTGGAA	4739
QY		4621	GAGTCTGGGCCACACGATTTTGAACGGAACATCTTACTTGGCCAGGCCAAGATCTAGAGGGA	4680
DB		4740	GAGTCTGGGCCACACGATTTTGAACGGAACATCTTACTTGGCCAGGCCAAGATCTAGAGGGA	4799
QY		4681	ACCCCTTACCTGGATCTGGNAATCAGCCTCTTCTCTGATGACCCCTGAATCTGATCTCTCT	4740
DB		4800	ACCCCTTACCTGGATCTGGNAATCAGCCTCTTCTCTGATGACCCCTGAATCTGATCTCTCT	4859
QY		4741	GAAGACAGAGCCCCAGAGTCAGCTCGTGTGGCAACATACATCTTCAACCTCTGCATTTG	4800

	Db	4860	GAAACAGAGCCCGAGAGTCGCTGGTGTGGCAACATACCNTCTTCAACCTCTGCATTG	4919
Qy	4801	AAGGTTCCCAAATTGAAGAATTGCAGAAATCGCCCAAGGCTCAGCTGCTGCTCATACTACT	4860	
Db	4920	AAGGTTCCCAAATTGAAGAATTGCAGAAATCTGCCAAGGTCAGTGCTCATCTACT	4979	
Qy	4861	GATACTGCTGGGTATTAATGCATATGGAAGATGTGACGAGGGAAGACCGAATTTGACA	4920	
Db	4980	GATACCTGCTGGGTATTAATGCAATTTGGAAGAAGATGTGACGAGGGAAGACCGAATTTGACA	5039	
Qy	4921	GCTTCAACAGAAAAGGGTCAACAAAAAGATGTCCATGTGTGTGTCTGGCCCTGACCCACAGAA	4980	
Db	5040	GCTTCAACAGAAAAGGGTCAACAAAAAGATGTCCAATGTGTGTGTCTGGCCCTGACCCACAGAA	5099	
Qy	4981	GAATTTATGCTCGTGTAACAAGTTGCCAGAAAAACAACAATCACTTTTAACATACTTAATTT	5040	
Db	5100	GAATTTATGCTCGTGTAACAAGTTGCCAGAAAAACAACAATCACTTTTAACATACTTAATTT	5159	
Qy	5041	ACTGAAGAGACTACTCATATGTTGTTATGAAAAACAGATGCTGAGTTGTGTGTGAACCGACA	5100	
Db	5160	ACTGAAGAGACTACTCATATGTTGTTATGAAAAACAGATGCTGAGTTGTGTGTGAACCGACA	5219	
Qy	5101	CTGAATATTTTTCTAGAAATTCGGGAGGAAAAATGGTAGTTAGCTATTTCTCGGTGACC	5160	
Db	5220	CTGAATATTTTTCTAGAAATTCGGGAGGAAAAATGGTAGTTAGCTATTTCTCGGTGACC	5279	
Qy	5161	CAGTCTATTTAAAGAAAGAAAAATGCTGAATGAGCATGATTTTGAAGTCTGAGAGAGATGTG	5220	
Db	5280	CAGTCTATTTAAAGAAAGAAAAATGCTGAATGAGCATGATTTTGAAGTCTGAGAGAGATGTG	5339	
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Qy	5521	AGTGTAGCACTTACCAAGTCCAGGAGCTGGACACCTTACCTGTATACCCAGATCCCCAC	5580	
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LOCUS	I59546			
DEFINITION	Sequence 1 from patent US 5654155.	5711 bp	DNA	linear PAT 07-OCT-1997
ACCESSION	I59546			
VERSION	I59546.1 GI:2478178			

RESULT 5

159546

LOCUS

DEFINITION:

ACCBSSION
ITERATION

VERSTION
VERBODING

AS I WOULD
SOURCE

ORGANIS

.....

REFERENCE

AUTHORS

Accession	Length	Source	Feature	Accession
I59546	5711 bp	DNA	linear	PAT 07-OCT-1997
Sequence 1 from patent US 5654155.				

known

Unknown.

Unclassified.

1 (bases 1 to 5711)
Murphy, P.D., Allen, A.C., Alvares, C.P., Critz, B.S., Olson, S.J.,
Scheller, D.B. and Zeng, B.

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RESULT 6
AR007334
LOCUS AR007334
DEFINITION Sequence 3 from patent US 5750400.
ACCESSION AR007334
VERSION AR007334.1 GI:3966818
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5711)
AUTHORS Murphy,P.D., Allen,A.C., Alvares,C.P., Critz,B.S., Olson,S.J.,
Schelter,D.B. and Zeng,B.
TITLE Coding sequences of the human BRCA1 gene
JOURNAL -Patent- US 5750400-A 3 12-MAY-1998;
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source
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ORIGIN
Query Match 99.9%; Score 5581; DB 6; Length 5711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5584; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 3360 AATGCTATGCTTAGATTTAGGCTTTTGCACCTGAGGCTATATAACAAGTCTTCTCTGGA 3419
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RESULT 7	AR112810	5711 bp	DNA	linear	PAT 16-MAY-20001
LOCUS	AR112810				
DEFINITION	Sequence 5 from patent US 6130322.				
ACCESSION	AR112810				
VERSION	AR112810.1	GI:14092710			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 5711)				
	Murphy, P.D., Allen, A.C.P., Alvarez, C.P., Critz, B.S., Olson, S.J.,				

Thurber, D. and Zeng, B.
Coding sequences of the human BRCA1 gene
Patent: US 6130322-A 5 10-OCT-2000;
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ORIGIN

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SOURCE Unknown.
ORGANISM Unclassified.
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AUTHORS Mismatch endonuclease and its use in identifying mutations in
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ORIGIN

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LOCUS	VERSION
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Sequence 15 from Patent WO02100897.
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AX659576.1 GI:29161780

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AUTHORS	dalla Venezia,N., Megnard,C., Lenoir,G. and Similnikova-Brard,O.	
TITLE	Brcal/acc alpha molecular complexes, diagnostic and therapeutic applications	
JOURNAL	Patent: WO 0210897-A 15 19-DEC-2002;	
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RESULT 10

HSU14680
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

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Homo sapiens breast and ovarian cancer susceptibility (BRCA1) mRNA,
complete cds.
U14680.1 GI:555931
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Miki, Y., Svendsen, J., Shattuck-Eidens, D., Futreal, P.A., Harshman, K.,
Tavtigian, S., Liu, Q., Cochran, C., Bennett, L.M., Ding, W., Bell, R.,
Rosenthal, J., Huseby, C., Tran, T., McClure, M., Frye, C., Hattier, T.,
Phelps, R., Haugen-Strano, A., Katcher, H., Yakumo, K., Gholami, Z.,
Shaffer, D., Stone, S., Bayer, S., Wray, C., Bogden, R., Dayananth, P.,
Ward, J., Tonin, P., Narod, S., Bristow, P.K., Norris, F.H.,
Helvering, L., Morrison, P., Rostock, P., Lai, M., Barrett, J.C.,
Lewis, C., Neuhausen, S., Cannon-Albright, L., Goldgar, D., Wiseman, R.,
Kamb, A. and Skolnick, M.H.
A strong candidate for the breast and ovarian cancer susceptibility
gene BRCA1

TITLE

Science 266 (5182), 66-71 (1994)

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLES

JOURNAL

FEATURES

source

Location/Qualifiers

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GenBank Accession Number U15595"

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QY 781 TATCAGGATAGTTCGTTTTCAAACTTGCATGTGAGGCACTGTGGCACAAATCTCATGCC 840
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QY 900 TATCAGGATAGTTCGTTTTCAAACTTGCATGTGAGGCACTGTGGCACAAATCTCATGCC 959
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Db |||||

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4860 GAGGACAGAGGCCCCAGAGTCTGCTGCTTGGCAACATACCATCTTCAACCTCTGCAATG 4919
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Db	3240	TC	AAGCAATATTAATGAAGTAGGTTCCAGTACTAAATGAAGTGGGCTCCAGTATTAATAGAA	3299
Qy	3181	AT	AGGTTCCAGTGAATGAAAAATTC	3240
Db	3300	AT	AGGTTCCAGTGAATGAAAAATTC	3359
Qy	3241	AATGCTAATGCTTATGATTTAGGGGTTTGCAACCTGAGGCTATATAAA	3300	
Db	3360	AATGCTATGCTTATGATTTAGGGGTTTGCAACCTGAGGCTATATAAA	3419	
Qy	3301	AGTAATTTGAAGCATCTCTGAAATAAAAAACAAGATATCAAGAGTAGTTACAGACTGTT	3360	
Db	3420	AGTANTTGAAGCATCTCTGAAATAAAAAACAAGATATCAAGAGTAGTTACAGACTGTT	3479	
Qy	3361	AATACAGATTCTCTCCATATCTGATTTACAGATAAATTTAGAACGCTATATGGAAAGTAGT	3420	
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Qy	3421	CATGCATCTCAGGTTGTTCTGAGACACCTGTATGACCTGTTAGATGATGTAATAAAG	3480	
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Qy	3541	GTCCAGAGAGGAGGCTTAGCAGAGTCTAGACCTTACCCATACACANTTTGGCTCAG	3600	
Db	3660	GTCCAGAGAGGAGGCTTAGCAGAGTCTAGACCTTACCCATACACANTTTGGCTCAG	3719	
Qy	3601	GGTTACCCAGAGGGGCCAAAGAAATTAGAGTCTCTCAGAGAGAACTTATCTAGTAGGAT	3660	
Db	3720	GGTTACCCAGAGGGGCCAAAGAAATTAGAGTCTCTCAGAGAGAACTTATCTAGTAGGAT	3779	
Qy	3661	GAAGAGCTTCCCTGCTTCCAAACACTTGTTATTTGGTAAAGTAAACAATATACCTTCTCAG	3720	
Db	3780	GAAGAGCTTCCCTGCTTCCAAACACTTGTTATTTGGTAAAGTAAACAATATACCTTCTCAG	3839	
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Db	3840	TCTACTAGGCATAGCACCGTTGCTTACCGAGTGCTGTCTAAGAAACACAGAGGAGAAATTTA	3899	
Qy	3781	TTATCATTTGAAGAAATAGCTTAAATGACTGCAGTAACACAGGTAATATTTGGCAAGGCATCT	3840	
Db	3900	TTATCATTTGAAGAAATAGCTTAAATGACTGCAGTAACACAGGTAATATTTGGCAAGGCATCT	3959	
Qy	3841	CAGGAACATCACCTTAGTGAGGAAACAAATGTTCTGCTAGCTTGTTTTCTTACAGTGC	3900	
Db	3960	CAGGAACATCACCTTAGTGAGGAAACAAATGTTCTGCTAGCTTGTTTTCTTACAGTGC	4019	
Qy	3901	AGTGAATTTGAAGAACTTGACTGCAATATACAAACACCCAGGATCCTTTCTTGGATTGGTTCT	3960	
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Qy	3961	TCCAAACAAATATAGGCATCTAGTCTGAAGACCGAGGATTTGGTCTGAGTGACAGGAATTG	4020	
Db	4080	TCCAAACAAATATAGGCATCTAGTCTGAAGACCGAGGATTTGGTCTGAGTGACAGGAATTG	4139	
Qy	4021	GTTTTCAGATATGAAGAAAGAGGAAACGGGCTTTGGAAGAAAAATATCAAGAGAGCAAAAGC	4080	
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Qy	4081	ATGGATTCAAATTTAGTGTAAGCAATCTGGGTGTGAGAGTGAAACAAGCGTCTCTGAA	4140	
Db	4200	ATGGATTCAAATTTAGTGTAAGCAATCTGGGTGTGAGAGTGAAACAAGCGTCTCTGAA	4259	
Qy	4141	GACTGCTCCGGGCTATCCTCTCAGAGTGACATTTTAAACCCTCAGCAGAGGGATACCATG	4200	
Db	4260	GACTGCTCCGGGCTATCCTCTCAGAGTGACATTTTAAACCCTCAGCAGAGGGATACCATG	4319	
Qy	4201	CAACATTAACCTGATAAAGCTCCAGCAGGAATGGCTGAACCTAGAGGCTGTGTTAGAACAG	4260	

4320	Db	CAACATAACCTGATAAGCTCCAGCAGGAAATGGCTGAACTAGAGCTGTGTTAGAACAG	4379
4261	Qy	CATGGGAGCAGGCTTTCTAAACAGCTACCTTCATATAAGTGACTTCTCTGCGCTTGAG	4320
4380	Db	CATGGGAGCAGGCTTTCTAAACAGCTACCTTCATATAAGTGACTTCTCTGCGCTTGAG	4439
4321	Qy	GRCTCGGAANTCCAGAACAAAGACCATCAGAAAAAGCAGTATTAACTTTCACAGAAAAAGT	4380
4440	Db	GACTCGGAANTCCAGAACAAAGACCATCAGAAAAAGCAGTATTAACTTTCACAGAAAAAGT	4499
4381	Qy	AGTGAATACCTTATAAGCCAGGAATCCAGAGGCGCTTTCTGCTGACAAAGTTTGAGGTGTCT	4440
4500	Db	AGTGAATACCTTATAAGCCAGGAATCCAGAGGCGCTTTCTGCTGACAAAGTTTGAGGTGTCT	4559
4441	Qy	GCAGATAGTTCTACACGATAAAAATAAGAACACGAGAGTGGAAAGGTCATCCCTCTCTAAA	4500
4560	Db	GCAGATAGTTCTACACGATAAAAATAAGAACACGAGAGTGGAAAGGTCATCCCTCTCTAAA	4619
4501	Qy	TGCGCATCATTAGATGATAGGTGGTACATGCACAGTTGCTCTGGGAGTCTTCAGAATAGA	4560
4620	Db	TGCGCATCATTAGATGATAGGTGGTACATGCACAGTTGCTCTGGGAGTCTTCAGAATAGA	4679
4561	Qy	AATACCCATCTCAGAGGAGTCATTAAGTTGTTGATGTGGAGAGCAACAGCTGGAA	4620
4680	Db	AATACCCATCTCAGAGGAGTCATTAAGTTGTTGATGTGGAGAGCAACAGCTGGAA	4739
4621	Qy	GAGTCTGGGGCCACACCATTTGACGGAAACATCTTACTTGCACAGGCAAGATCTAGAGGGA	4680
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4800	Db	ACCCCTTACCTGGAATCTCGAATCAGCCTCTTCTCTGATGACCCCTGAATCTGATCTCTCT	4859
4741	Qy	GAAGACAGAGCCCGCAGCTCGCTGTTGTGGCAAATACATCATCTTCAACCTCTGCAATTG	4800
4860	Db	GAAGACAGAGCCCGCAGCTCGCTGTTGTGGCAAATACATCATCTTCAACCTCTGCAATTG	4919
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4980	Db	GATACTCTGGGTATAATGCAATGGAAGAAGTTGAGCGAGGAGAGCCAGAAATTGACA	5039
4921	Qy	GCCTTCAACAGAAAGGGTCAACAAAGAAATGTCATGGTGGTGTCTGGCTGACCCCGAGAA	4980
5040	Db	GCCTTCAACAGAAAGGGTCAACAAAGAAATGTCATGGTGGTGTCTGGCTGACCCCGAGAA	5099
4981	Qy	GAATTTATGCTCGTGATCAAGTTTGCAGAAACACCAATCATCTTTAACTATCTAATT	5040
5100	Db	GAATTTATGCTCGTGATCAAGTTTGCAGAAACACCAATCATCTTTAACTATCTAATT	5159
5041	Qy	ACTGAAGAGACTACTCATGTTGTTATGAAACAGATGCTGAGTTGTGTGTGAACGGACA	5100
5160	Db	ACTGAAGAGACTACTCATGTTGTTATGAAACAGATGCTGAGTTGTGTGTGAACGGACA	5219
5101	Qy	CTGAATATTTTCTAGGAATTCGGGAGGAAATGGGTAGTTAGCTATTTCCTGGGTGACC	5160
5220	Db	CTGAATATTTTCTAGGAATTCGGGAGGAAATGGGTAGTTAGCTATTTCCTGGGTGACC	5279
5161	Qy	CAGTCTATTAAAGAAAGAAATGCTGAAATGAGCATGATTTTGAAGTTCAGAGGAGATGTG	5220
5280	Db	CAGTCTATTAAAGAAAGAAATGCTGAAATGAGCATGATTTTGAAGTTCAGAGGAGATGTG	5339
5221	Qy	GTCAATGGAAAGAAACCAACCAAGGTCCAAAGCGCAGCAGAGAAATCCCGAGCAGAAAGATC	5280
5340	Db	GTCAATGGAAAGAAACCAACCAAGGTCCAAAGCGCAGCAGAGAAATCCCGAGCAGAAAGATC	5399
5281	Qy	TTCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTCCACCAATGTCGCCACAGATCAACTG	5340

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RESULT 12
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DEFINITION
ACCESSION
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SOURCE
ORGANISM

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ACCESSION AR184044
VERSION AR184044.1 GI:20228013
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5712)
AUTHORS Holt, J. T., Jensen, R. A., Page, D. L., Obermiller, P. S.,
Robinson-Benion, C. L. and Thompson, M. E.
TITLE Method for detection and treatment of breast cancer
JOURNAL Patent: US 6342483-A 47 29-JAN-2002;
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Query March 99.8%; Score 5579.4; DB 6; Length 5712;
Best Local Similarity 99.9%; Pred. No. 0;
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ACCESSION AR004673
VERSION AR004673.1 GI:3965552
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 5914)
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AUTHORS

Skolnick, M.H., Goldgar, D.E., Miki, Y., Swenson, J., Kamb, A.,
Harshman, K.D., Shattuck-Eidens, D.M., Tavtigian, S.V., Wiseman, R.W.
and Putreal, P. Andrew
17Q-linked breast and ovarian cancer susceptibility gene

TITLE

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JOURNAL

Location/Qualifiers

FEATURES

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ORIGIN

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3360 AATGCTATGCTTAGATTAGGGGTTTGGACCTGAGGTCTATTAACAAAGTCTTCTCGGA 3419
3301 AGTAAATTGTAAGCATCTGAAATTAAGAAAGCAAGAAATATGAAGAGTAGTTCAAGCTGT 3360
3420 AGTAAATTGTAAGCATCTGAAATTAAGAAAGCAAGAAATATGAAGAGTAGTTCAAGCTGT 3479
3361 AATACAGATTCTCTCATATCTGATTTAGATAAATTTAGATAAATTTAGATAAATTTAGATAA 3420
3480 AATACAGATTCTCTCATATCTGATTTAGATAAATTTAGATAAATTTAGATAAATTTAGATAA 3539
3421 CATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGATGATGATGATGAT 3480
3540 CATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGATGATGATGATGAT 3599
3481 GAAGATATCTAGTTTGTCTGAAATGATCAATTAAGGAAAGTTCTGCTGTTTTTATGCAAAAGC 3540
3600 GAAGATATCTAGTTTGTCTGAAATGATCAATTAAGGAAAGTTCTGCTGTTTTTATGCAAAAGC 3659
3541 GTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3600
3660 GTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3719
3601 GGTATCCGAAAGAGGGGCCAAGAAATTTAGAGTCTCTCAGAGAGAACTTTATCTAGTGAAGAT 3660
3720 GGTATCCGAAAGAGGGGCCAAGAAATTTAGAGTCTCTCAGAGAGAACTTTATCTAGTGAAGAT 3779
3661 GAAGAGTCTCCGCTGCTTCCAACTTTGTTATTTGGTAAAGTAAACAAATATATCTCTCAG 3720
3780 GAAGAGTCTCCGCTGCTTCCAACTTTGTTATTTGGTAAAGTAAACAAATATATCTCTCAG 3839
3721 TCTACTAGGATAGCAGCCGTTGCTACCGAGTGTCTGCTAAGAGAACACAGAGAGAGATTTA 3780
3840 TCTACTAGGATAGCAGCCGTTGCTACCGAGTGTCTGCTAAGAGAACACAGAGAGAGATTTA 3899
3781 TTATCATTTGAAGATAGCTTAATGATCTGAGTAAACCAAGTAAATTTGGCAAGGCACTCT 3840
3900 TTATCATTTGAAGATAGCTTAATGATCTGAGTAAACCAAGTAAATTTGGCAAGGCACTCT 3959
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4800 ACCCTTACTCTGGAATCTGGAATCAGCTCTTCTCTGATGAGCCCTGGAATCTGATCTCTCT 4859
4741 GAAGACAGAGGCCACAGATCTGAGTCTGTTGGCAACATACATCTTCAACCTCTGCAATG 4800
4860 GAAGACAGAGGCCACAGATCTGAGTCTGTTGGCAACATACATCTTCAACCTCTGCAATG 4919
4801 AAGGTTTCCCAATTTGAAAGTTGCAAGTCTGCCAGGGTCCAGCTGCTGCTCATACTACT 4860
4920 AAGGTTTCCCAATTTGAAAGTTGCAAGTCTGCCAGGGTCCAGCTGCTGCTCATACTACT 4979
4861 GATACCTGCTGGGTATTAATGCAATGGAAGAAAGTGTGAGCAGGAGGAGGAGGAGGAGGAGGAG 4920
4980 GATACCTGCTGGGTATTAATGCAATGGAAGAAAGTGTGAGCAGGAGGAGGAGGAGGAGGAGGAG 5039
4921 GCTTCAACAGAGAGGCTCAACAAAGAGATGCTCAATGGTGTGCTGCTGCTGCTGCTGCTGCTGCT 4980
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5221 GTCATGAGAGAAACCAACCAAGGTTCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5280

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 11, 2004, 19:58:38 ; Search time 13193 Seconds

(without alignments)
12926.773 Million cell updates/sec

Title: US-09-734-672A-3

Perfect score: 5711

Sequence: 1 AGCTCGTGAGACTTCCTGG.....TCCGCCACAGCACTACTGA 5711

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

RST:*
1: em estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmi.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
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11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
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17: em_gss_hum.*
18: em_gss_inv.*
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21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
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27: em_gss_vrl.*
28: gb_gss1.*
29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2061.4	36.1	2101	11 BC012577	BC012577 Homo sapi
2	2055.6	36.0	2090	11 BC030969	BC030969 Homo sapi
3	1416.4	24.8	1578	11 BC038947	BC038947 Homo sapi
4	968.8	17.0	1919	11 AK086173	AK086173 Mus muscu

5	863	15.1	962	13	BQ068830
6	841.4	14.7	1089	12	BM452288
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8	760.2	13.3	783	9	AU142729
9	750.6	13.1	789	14	CK000353
10	746.4	13.1	933	13	BUI171200
11	738.8	12.9	743	12	BQ681276
12	734.6	12.9	899	13	BQ422380
13	706.2	12.4	878	13	BQ215100
14	701.2	12.3	739	14	CF121736
15	698	12.2	856	13	BUI14744
16	688	12.0	702	9	AU125312
17	687.6	12.0	747	12	BG777447
18	686.6	12.0	739	10	BF508987
19	686.4	12.0	987	12	BM800251
20	658.6	11.5	900	10	BF791668
21	651.6	11.4	938	12	BG257190
22	639	11.2	675	9	AL704228
23	631	11.0	631	14	CB155501
24	617.6	10.8	921	12	BG178466
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29	593	10.4	933	13	BQ683955
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31	591	10.3	724	9	AI915085
32	591	10.3	800	10	BF794879
33	586	10.3	947	13	BQ679749
34	582.8	10.2	949	13	BUI155689
35	581	10.2	910	13	BQ677666
36	580.4	10.2	941	13	BUI163307
37	575	10.1	602	10	BE043393
38	548.2	9.6	638	12	BM042282
39	541.8	9.5	546	14	CB118225
40	535.2	9.4	638	10	BE264293
41	530	9.3	563	10	AW295197
42	528.6	9.3	585	10	AW968546
43	528	9.2	528	14	CB158976
44	516.4	9.0	666	10	AW968720
45	498.2	8.7	509	10	AW504244

ALIGNMENTS

RESULT 1	BC012577	BC012577	Homo sapiens, clone IMAGE:3996658, mRNA.	2101 bp	mrna	linear	HTC 04-MAR-2003
LOCUS	BC012577	Homo sapiens, clone IMAGE:3996658, mRNA.					
DEFINITION	BC012577	Homo sapiens, clone IMAGE:3996658, mRNA.					
ACCESSION	BC012577	Homo sapiens, clone IMAGE:3996658, mRNA.					
VERSION	BC012577.1	GI:15214876					
KEYWORDS	HTC.						
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
REFERENCE	1 (bases 1 to 2101)						
AUTHORS	Strausberg, R.						
TITLE	Direct Submission						
JOURNAL	Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA						
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov						
COMMENT	Contact: MGC help desk Email: gcaps-rc@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbio.org contact: amadansystemsbiology.org						


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1805 DB CTAATTCAGAAATGAGAAAAATCTAAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA 1864
1861 QY AAAACGAAAGCTCAACCTATAAGCAGCAGTATTAAGCAATATGAATTCGAAATTTAAATATCC 1920
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1921 QY ACAATTCAAAAGCACTAAAAGAAATAGCTCAGAGGAAAGTCTTCTACAGGCAATATTC 1980
1925 DB ACAATTCAAAAGCACTAAAAGAAATAGCTCAGAGGAAAGTCTTCTACAGGCAATATTC 1984
1981 QY ATGCGCTTGAACCTAGTACGTAGCAATCTAAGCCCACTAATTTGACTGAATTCGAAA 2040
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2045 DB TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACAAA 2095

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RESULT 2
BC030969
LOCUS
DEFINITION
Homo sapiens, similar to breast cancer 1, early onset, clone
IMAGE:4804551, mRNA.
ACCESSION
BC030969.1 GI:21411299
VERSION
BC030969.1
KEYWORDS
HTC.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2090)
Strausberg,R.
Direct Submission
Submitted (03-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapps-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

```

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Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LILNL at: http://image.llnl.gov
Series: IRAL Plate: 41 Row: P Column: 11
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6552298
This clone has the following problem: frame shifted.
FEATURES
Location/Qualifiers
1..2090
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4804551"
/tissue_type="Prostate, adenocarcinoma."
/clone_lib="NIH MGC_60"
/lab_host="pH10B"
/note="Vector: pDNR-LIB"

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ORIGIN
Query Match 36.0%; Score 2055.6; DB 11; Length 2090;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2075; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

```

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2 AGCTCGCTGAGACTTCTTGGA CCGCCAGAGCTGTGGGTTTCTCAGATAACTGGGCC 60
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61 CCTCGCTCAGAGGCTTCA CCGCTCTGCTCTGGTTAAAGTTCAATCGACAGAAAGAAA 120
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121 TGGATTATCTGCTCTTTCGGGTTGAGAGAGTACAAAATGTCAATTAATGCTATGACAGAAA 180
181 TCTTAGAGTGTCCCATCTGCTCTGAGTGTGATCAAGGAACTGTCTCCAAAAGTGTGACC 240
181 TCTTAGAGTGTCCCATCTGCTCTGAGTGTGATCAAGGAACTGTCTCCAAAAGTGTGACC 240
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241 ACATATTTTGC AAAATTTTGCATGCTGAAACTTCTCAACCAGAGAAAGGGGCTTCA CAGT 300
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301 GTCCTTTATGTAAGATGATATAACCAAAAGGAGCCTACAAAGAAAGTACGAGATTGATC 360
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Db 1381 AATATTCTGTTCTTTCAGAGAAATAGACTTACTGCGCAGTGTACTCTCATGAGGCTTTAA 1440
QY 1441 TATGTTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGATTAATATTGAAGCAAAATAT 1500
Db 1441 TATGTTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGATTAATATTGAAGCAAAATAT 1500
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QY 1561 TAAATTAGAGCAATTTGTTACTGAGCCACAGATTAACAAGAGCGTCCCTCCACAAATA 1620
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Db 1921 ACAATTCAGAGCAGCTTAAGAGATAGCTGAGGAGAGTCTTCTACCGAGCATTC 1980
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RESULT 3

BC038947

LOCUS

DEFINITION Homo sapiens, similar to breast cancer 1, early onset, clone

BC038947

1578 bp

mRNA

linear

HTC 04-MAR-2003

ACCESSION

BC038947

VERSION

BC038947.1

KEYWORDS

HTC

SOURCE

Homo sapiens

ORGANISM

Homo sapiens (human)

REFERENCE

Strausberg, R.

AUTHORS

Direct Submission

TITLE

Submitted (01-NOV-2002)

JOURNAL

National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

REMARK

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc_mgc@nsl.nih.gov

Akter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,

Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,

Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,

Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,

McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,

Tsurgren, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,

Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAP Plate: 82 Row: 9 Column: 3

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 6552304

This clone has the following problem: retained intron.

FEATURES

Location/Qualifiers

1..1578

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5531286"

/tissue_type="Uterus, leiomyosarcoma"

/clone_id="NIH_MGC_71"

/lab_host="DH10B"

/note="vector: pCW-SPORT6"

ORIGIN

Query Match

Best Local Similarity 24.8%; Score 1416.4; DB 11; Length 1578;

Matches 1563; Conservative 0; Mismatches 1; Indels 126; Gaps 2;

QY 391 GTGCTTTTCAGCTTGACACAGGTTTGGAGTATGCAACAGCTATAATTTTGCAGAAAAGG 450

Db 12 GTGCTTTTCAGCTTGACACAGGTTTGGAGTATGCAACAGCTATAATTTTGCAGAAAAGG 71

QY 451 AAATAAATCTCTCGACATCAAAAGATGAAGTTTCTATCATCCCAAGTATGGCTACA 510

Db 72 AAATAAATCTCTCGACATCAAAAGATGAAGTTTCTATCATCCCAAGTATGGCTACA 131

QY 511 GAAACCGTGCAGAAAGACTTCTACAGAGTGAACCCGAAATCTCTTCTTGCAGGAAACCA 570

Db 132 GAAACCGTGCAGAAAGACTTCTACAGAGTGAACCCGAAATCTCTTCTTGCAGGAAACCA 188

QY 571 GTCTCAGTGTCCAACTCTCTAACTTGGAACTGTGAGAACTCTGAGGACAAAGCAGCGGA 630

Db 189 GTCTCAGTGTCCAACTCTCTAACTTGGAACTGTGAGAACTCTGAGGACAAAGCAGCGGA 248

QY 631 TACAACCTCAAAAGACGCTGTCTATCATTTGAATTTGGATCTTCTGTAAGATACCG 690
 DB 249 TACAACCTCAAAAGACGCTGTCTATCATTTGAATTTGGATCTTCTGTAAGATACCG 282
 QY 691 TTAATAAGGCAACTTATTGCACTGTGGGAGATCAAGAATTGTTACAAATCACCCTCAAG 750
 DB 283 ----- 282
 QY 751 GAACAGGGATGAATATCAGTTTGGATTCGCAAAAAGCGCTGTGTGAATTTCTGAGA 810
 DB 283 -----GGCTGCTGTGAATTTCTGAGA 305
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 DB 306 CGGTGTACCAATATCTGACATCATCAACCACTCAATTAATGATTTGAACCACTGAGA 365
 QY 871 AGCGTGCAGCTGAGAGGATCCAGAAAAGTATCAGGCTAGTTCTGTGTTCAAACTTGCATG 930
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DB 1206 TGATAAATCAGGGAACCTAAACCAACCGAGCAGATGGTCAAGTATGATTAATTAATA 1265
 QY 1771 GTGGTCAATGAGAAATAAAACAAAGAGTCTATTTCAAGATGAGAAAATCTCTAACCCAA 1830
 DB 1266 GTGGTCAATGAGAAATAAAACAAAGAGTCTATTTCAAGATGAGAAAATCTCTAACCCAA 1325
 QY 1831 TAGAATCACTCGAAAAAGATCTGCTTTTCAAAAGCAAGCTGAACCTTATTAAGCAGAGTA 1890
 DB 1326 TAGAATCACTCGAAAAAGATCTGCTTTTCAAAAGCAAGCTGAACCTTATTAAGCAGAGTA 1385
 QY 1891 TAACCAATGGAACCTCGAATTAATAATCCACAAATTCAAAAGCAACCTTAAAGAAATAGGC 1950
 DB 1386 TAACCAATGGAACCTCGAATTAATAATCCACAAATTCAAAAGCAACCTTAAAGAAATAGGC 1445
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 DB 1446 TGAGGAGGAAGTCTTCTTACCAGGCATATTCATGCTTGAACCTAGTAGTAGTAAATC 1505
 QY 2011 TAAGCCACCTATTTGCTGCAATTCGAATTCGAATTCGATTCCTAGCAGTGAAGAGATAA 2070
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 DB 1566 AAAAAAAA 1575

RESULT 4
 AK086173
 LOCUS
 DEFINITION
 1919 bp mRNA linear HTC 20-SEP-2003
 Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930010H15 product:brest cancer 1, full insert sequence.
 ACCESSION
 AK086173
 VERSION
 AK086173.1 GI:26103274
 KEYWORDS
 HTC; CAP trapper.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 1
 Carninci, P. and Hayashizaki, Y.
 TITLE
 High-efficiency full-length cDNA cloning
 JOURNAL
 Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE
 99279253
 PUBMED
 10349636

REFERENCE
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL
 Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE
 20499374
 PUBMED
 11042159

REFERENCE
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 JOURNAL
 Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE
 20530913
 PUBMED
 11076861

REFERENCE
 4
 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 TITLE
 Functional annotation of a full-length mouse cDNA collection
 JOURNAL
 Nature 409, 685-690 (2001)

	Qy	297	CAGTGTCTTTATGTAAGAATCATATAACCAAAAGGAGCCTACAGAAAGTACGAGATT	355
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	Qy	537	AGTGAAACCGGAAAATCTCTTCTTGACGAAACCAGTCTCAGTGTCCAATCTCTTAACTTT	596
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	Qy	837	CAACCAAGTAATTAATGTTTGAACCACTGAGAGCGTGGAGCTGAGAGGATCCAGAA	896
	Dd	831	CAATGAGC--TGATGATTTAAACCTTACTGAGATCAATGCAATGGAAGGATCCAGAA	887
	Qy	897	AAGTATCAGGCTAGTTCTCTTTTCAAACTTGCATTTGGAGCCATGTTGGCACAATACTCAT	956
	Dd	888	AAATGTCAAGATTTTCTTCTTCTTCAATGTTGTTGTTGGAGCCATGTTGGCACAATACTCAT	947
	Qy	957	GCAGTCTCAATTAAGCAGATGAGAAACAGAGTATTATCTCACTAATAAGACAGATGAATGTA	1015
	Dd	948	GCCAGCTCAATTAAGCAGATGAGAAACAGAGTATTATCTCACTAATAAGACAGATGAATGTA	1000
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	Dd	1008	GAAGAGGCTGAATTTCTGTAATAAAGCAACAGCGCTGTAGCAAGGAGGACCAACATTAAC	1066
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	Qy	1377	GATGAATATTTCTGTTTCTTACAGAGAAATPAGATTTACTTGGCCAGTGATCTCTATGAGCT	1436

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420: 563-573 (2002)

6 (bases 1 to 1919)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagata, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komori, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, K., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, E., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/

URL: http://phantom.gsc.riken.go.jp/

Location/Qualifiers

1..1919

/organism="Mus musculus"

/mol_type="mRNA"

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Best Local Similarity 73.5%; Pred. No. 1.7e+209;

Matches 1384; Conservative 0; Mismatches 387; Indels 113; Gaps 7;

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146 GTCTCTGGCGCTGGAAAGTACGATCTTTTCTGGAGAAAGTTCACTGCACTGGA 205

117 GAATGATGATTTATCTCTCTCGCTTGAAGAGTACAAAATGTCATTAATGCTATGCGAG 176

206 GAATGATGATTTATCTCGCGCTCAAAATTCGAAGAGTACAAAATGTCCTTCATGCTATGCGAG 265

177 AAATCTCTAGAGTGTCCCATCTCTCTGCGAGTTGATCAAGGAACTGTCTCCCAAAAGTGT 236

266 AAAATCTTAGAGTGTCCGATCTCTTGGAACTGATCAAGAAAGCTGTTTCCACAAAGTGT 325

237 GACCAATATTTTGGAAAATTTGATGCTGGAATCTTCAACCAAGAGAAAGGGCTTCA 296

326 GACCAATATTTTGGAAAATTTTGTATGCTGGAATCTTCTTAAACAGAGAAAGGGCTTCA 385

REFERENCE AUTHORS

JOURNAL</

Db 1368 GATGGGGTTTGTAGTCTTCAAGAAACAGAGCTAGTAACCCCGACCCCATCATCTACT 1427
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Qy 1914 AATATCCCAATTTCAAAAGCACCT 1937
Db 1896 AACGTCCACAGTTTCAAAAGCACCT 1919

RESULT 5
LOCUS BQ068830
DEFINITION AGENCOURT_6740238 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5802685
5', mRNA sequence.

ACCESSION BQ068830
VERSION BQ068830.1 GI:19897888
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 962)
NIH-MGC <http://mgs.cni.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.G.B. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2037 row: h column: 14
High quality sequence stop: 700.
Location/Qualifiers
1..962

FEATURES
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/clone="IMAGE:5802685"

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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_47"
/note="Organ: Brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 15.1%; Score 863; DB 13; Length 962;
Best Local Similarity 96.3%; Pred. No. 1.8e-185;
Matches 891; Conservative 0; Mismatches 32; Indels 2; Gaps 1;
Qy 4451 TCCAGAACAAAGCAGCATCAGAAAAAGCAGTAATTAATCTTCAGAAAAAGTAGTGAATACCC 4510
Db 15 TTCCGCGACGAGCCACATCAGAAAAAGCAGTAATTAATCTTCAGAAAAAGTAGTGAATACCC 74
Qy 4511 TATAGCCAGAAATCCAGAGGCCCTTCTGCTGCAAGTCTTGAAGTCTGAGAGTAGTTC 4570
Db 75 TATAGCCAGAAATCCAGAGGCCCTTCTGCTGCAAGTCTTGAAGTCTGAGAGTAGTTC 134
Qy 4571 TACAGTAAATAAAGAACACAGAGTGGAAAGTCTATCCCTTCTTAATGCCCATCAT 4630
Db 135 TACAGTAAATAAAGAACACAGAGTGGAAAGTCTATCCCTTCTTAATGCCCATCAT 194
Qy 4631 AGATGATAGTGGTACATGACAGTCTGCTGGAGTCTTCAGAAATAGAACTACCCATC 4690
Db 195 AGATGATAGTGGTACATGACAGTCTGCTGGAGTCTTCAGAAATAGAACTACCCATC 254
Qy 4691 TCAAGAGAGTCTCAATTAAGGTTGTTGATGTGGAGGAGCAACAGCTGGAAGAGTCTGGGCC 4750
Db 255 TCAAGAGAGTCTCAATTAAGGTTGTTGATGTGGAGGAGCAACAGCTGGAAGAGTCTGGGCC 314
Qy 4751 ACAGATTTGACGGAACATCTTACTTGCAGCAAGTCTAGAGGAGAACCCCTTACCT 4810
Db 315 ACAGATTTGACGGAACATCTTACTTGCAGCAAGTCTAGAGGAGAACCCCTTACCT 374
Qy 4811 GGAATCTGGAAATCAGCTCTTCTCTGATGACCTGATCTGATCTCTCTGAAGACAGC 4870
Db 375 GGAATCTGGAAATCAGCTCTTCTCTGATGACCTGATCTGATCTCTCTGAAGACAGC 434
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Qy 4931 ATTGAAAGTTGCAAGATCTGCCAGGTCAGGTCGCTGCTCATCTACTGATCTGCTGG 4990
Db 495 ATTGAAAGTTGCAAGATCTGCCAGGTCAGGTCGCTGCTCATCTACTGATCTGCTGG 554
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Db 555 TTATAATGCAATGGAAGAAAGTGTGAGCAGGAGAGGCAAGAAATTGACAGTTCAACAGA 614
Qy 5051 AAGGTCACAAAGAAATGTCATGTTGGTGTCTGGCTGACCCAGAGAAATTTATGCT 5110
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Qy 5171 TACTCATGTTGTTATGAAAAACAGATGCTGAGTGTGTGTGTAACCGACAGTGAATTTT 5230
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Qy 5231 TCTAGGAATTTGCGGAGGAAAAATGGGTAGTGTAGTCTATTTCTGGGTGACCCAGTCTATTA 5290
Db 795 TCTAGGAATTTGCGGAGGAAAAATGGGTAGTGTAGTCTATTTCTGGGTGACCCAGTCTATTA 854

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute

FEATURES

Location/Qualifiers
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ORIGIN

Query Match 14.2%; Score 811.8; DB 9; Length 845;
Best Local Similarity 99.1%; Pred. No. 8e-174;
Matches 336; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

QY 3819 GTAACATATACCTTCTCAGTCTACTAGGATAGCAGCGTTGCTACCGAGTGTCTGCT 3878
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DB 61 AAGAACACAGAGGAGATTTATTCATTGAAGATAGCTTAATGACTGCGAGTAACCG 120

QY 3939 GTAATATGGCAAGGCAATCTCAGGAACATACCTTAGTGAAGAAACAATGTTCTGCT 3998
DB 121 GTAATATGGCAAGGCAATCTCAGGAACATACCTTAGTGAAGAAACAATGTTCTGCT 180

QY 3999 AGCTGTGTTCTTCCACAGTCAATTTGAAGACTTGACTGCAAAATCAACACCCAG 4058
DB 181 AGCTGTGTTCTTCCACAGTCAATTTGAAGACTTGACTGCAAAATCAACACCCAG 240

QY 4059 GATCTCTTCTGATGTTCTTCCAAACAATGAGGCAATCAGTCTGAAAGCCAGGAGTT 4118
DB 241 GATCTCTTCTGATGTTCTTCCAAACAATGAGGCAATCAGTCTGAAAGCCAGGAGTT 300

QY 4119 GGTCTGAGTGACAGGAATGTTTTCAGATGATGAAGAGGAAAGCGGCTTGAAGAA 4178
DB 301 GGTCTGAGTGACAGGAATGTTTTCAGATGATGAAGAGGAAAGCGGCTTGAAGAA 360

QY 4179 AATAATCAAGAGAGCAAGCAATGCAATCAAACTTAGTGAAGCAAGCATCTGGGTGTGAG 4238
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QY 4239 AGTGAACACAGCGTCTTGAAGACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAACC 4298
DB 421 AGTGAACACAGCGTCTTGAAGACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAACC 480

QY 4299 ACTCAGCAGAGGATACCATGCAATCAATCAATGATAAGCTCCACAGCAAAATGCTGAA 4358
DB 481 ACTCAGCAGAGGATACCATGCAATCAATCAATGATAAGCTCCACAGCAAAATGCTGAA 540

QY 4359 CTAGAAGCTGTGTTAGAACAGCATGGGAGCCAGCGCTTCTTAACAGCTACCCCTTCCATCAT 4418
DB 541 CTAGAAGCTGTGTTAGAACAGCATGGGAGCCAGCGCTTCTTAACAGCTACCCCTTCCATCAT 600

QY 4419 AGTGACTCTTCTGCGCTTGAGGACCTGGGAATTCAGAACAGCAACACATCGAAGAAAGCA 4478
DB 601 AGTGACTCTTCTGCGCTTGAGGACCTGGGAATTCAGAACAGCAACACATCGAAGAAAGCA 660

QY 4479 GTATTAATCTTCAAGAAAAGTAGTGAATACCTTATAAGCCAGAAATCCAGAGCGCTTTCT 4538
DB 661 GTATTAATCTTCAAGAAAAGTAGTGAATACCTTATAAGCCAGAAATCCAGAGCGCTTTCT 720

QY 4539 GCTGACAGTTTGAGGTGCTCCAGATGTTCTTACAGTAAATAAAGAACACAGCA--G 4596
DB 4539 GCTGACAGTTTGAGGTGCTCCAGATGTTCTTACAGTAAATAAAGAACACAGCA--G 4596

Db 721 GCTGACAAAGTTTGAGGTGCTCTGACAGATAGTTCTTACCAGTAAAAAATNAAGAACACAGGAGT 780
QY 4597 TGGAAAGGTCA-TCCCTTCTTAATGCCATCATAGATAGTGTGTATCATGCACAGT 4655
DB 781 TGGAAAGGTCAATCCCTTCTTAATGCCATCATAGATAGTGTGTATCATGCACAGT 840
QY 4656 TGCT 4659
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RESULT 8

AU142729 783 bp mRNA linear EST 05-AUG-2002
LOCUS AU142729 Y79AA1 Homo sapiens cDNA clone Y79AA1000792 5', mRNA
DEFINITION sequence.
ACCESSION AU142729.1 GI:11004250
VERSION AU142729
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 783)
Ota, T., Mishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
Yanamoto, J., Wakamatsu, A., Nakamura, Y., Negai, T., Sugano, S. and
Isogai, T.
HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp

TITLE

JOURNAL

COMMENT

FEATURES

source

1..783
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/db_xref="taxon:9606"
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/cell_type="retinoblastoma"
/cell_line="Y79"
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Best Local Similarity 99.1%; Pred. No. 4.5e-162;
Matches 773; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 3579 TTGATGATGTTGAATTAAGGAGATAGTGTTCGTGAATGACATTAAGGAAAGT 3638
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QY 3639 TCTGCTGTTTTAGCAAAAGCGTCCAGAGAGGAGAGCTTAGCAGAGTCTTAGCCCTTTC 3698
DB 61 TCTGCTGTTTTAGCAAAAGCGTCCAGAGAGGAGAGCTTAGCAGAGTCTTAGCCCTTTC 120

QY 3699 ACCATACACATTTGGCTCAGGTTACCGAGAGGGGCCAGAAATTAGAGTCTCTCAGAA 3758
DB 121 ACCATACACATTTGGCTCAGGTTACCGAGAGGGGCCAGAAATTAGAGTCTCTCAGAA 180

QY 3759 GAGAACTTATCTAGTGAAGATGAAGAGCTTCCCTGCTTCCAACTTTGTTATTTGGTAAA 3818
DB 181 GAGAACTTATCTAGTGAAGATGAAGAGCTTCCCTGCTTCCAACTTTGTTATTTGGTAAA 240

QY 3819 GTAAACAATATACCTTCTCAGTCTACTAGGATAGCACCGTTGCTACCGAGTGTCTGCT 3878

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Db      241  GTAAACAATATACCTCTCAGTCTACTAGGCAATAGCACCGTTGTACCGAGTGTCTGTCT 300
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Qy      3939  GTAAATATTTGGCAAGGAGCTCTCAGAACATCACCTTACTAGTGGAGGAACCAAAATGTTCTGCT 3998
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Db      421  AGCTTGTGTTTCTTCACTGACGTGCAATTTGAAGACTTCTGACTGCAAAATACAAACACCCAG 480
Qy      4059  GATCCTTTCTTCAATGTTCTTCCAAACAATGAGGACGATCTGTAAGGACCGAGGATTT 4118
Db      481  GATCCTTTCTTCAATGTTCTTCCAAACAATGAGGACGATCTGTAAGGACCGAGGATTT 540
Qy      4119  GGTCTGAGTGAACAAGAAATGTTGTTTCAGATGATGAAGAAAGAGGAAACGGGCTTGGAGAA 4178
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Qy      4179  AATATCAAGAGACCAAGGCTGATTCATTAATTTAGTGAAGCACTCTGCGGTGTGAG 4238
Db      601  AATATCAAGAGACCAAGGCTGATTCATTAATTTAGTGAAGCACTCTGCGGTGTGAG 660
Qy      4239  AGTGAACAACAAGGCTCTGGAAGACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAA-C 4297
Db      661  AGTGAACAACAAGGCTCTGGAAGACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAAAC 720
Qy      4298  CACTCAGCAGAGGAGTACATGCAACATACCTGATAAGCTCCAGCAGGAAATGCGCTGA 4357
Db      721  CACTCAGCAGAGGAGTACATGCAACATACCTGATAAGCTCCAGCAGGAAATGCGCTGA 780

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RESULT 9

CK000353
 LOCUS AGENCOURT_16368380 NIH_MGC_220 Homo sapiens cDNA clone
 IMAGE:30706752 5', mRNA sequence.

ACCESSION

CK000353

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 789)

AUTHORS

NIH-MGC <http://mgi.nci.nih.gov/>

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: James Martin, University of Iowa
 cDNA Library Preparation: M. Bento Soares, University of Iowa
 DNA Sequencing by: The I.M.A.G.E. Consortium (ILLNL)
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILLNL at:
<http://image.llnl.gov>

Plate: NDA01070 row: e column: 01

High quality sequence stop: 713.

Location/Qualifiers

FEATURES

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1..789

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/clone="IMAGE:30706752"

/lab_host="DH10B fona"

/clone_lib="NIH_MGC_220"
 /note="Organ: mixed; Vector: pYX-Asc; Site 1: EcoRI;
 Site 2: NotI; Library is oligo-dT primed and directionally
 cloned. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to RNA size fraction, ligated with
 EcoR I adaptor, digested with Not I and then cloned
 directionally into pYX-Asc vector. Average insert size
 0.5-1kb. Adaptors 5' (AATTCGGCAGGAGG)3' and 5' (G
 CTTGCGGCG)3'. 3' linker sequence - GCGCCGCTGAGAGCC T18.
 Sequencing primers 3' end: T3 promoter primer 5' (A
 TTTAACCTCTCACTAAAGGA)3'. 5' End: T7 promoter primer 5' (A
 TTAATACGACTCACTATAGG)3'. Library was constructed in the
 laboratory of M. Bento Soares. Average insert size 3-4kb
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 13.1%; Score 750.6; DB 14; Length 789;
 Best Local Similarity 99.3%; Pred. No. 6.9e-160;
 Matches 764; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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 Db 5 AGGAGCACAAATTAGCGTAATAACATTAGAGAAATGTTTAAAGGACCGAGCTCAAG 64
 Qy 3245 CAATATTAAATGAAGTAGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAAATGAATAG 3304
 Db 65 CAATATTAAATGAAGTAGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAAATGAATAG 124
 Qy 3305 TTCCAGTGAGAAACATTTCAGCAGAACTAGCTGAGAAACAGAGGCGCAAAATGATGC 3364
 Db 125 TTCCAGTGAGAAACATTTCAGCAGAACTAGCTGAGAAACAGAGGCGCAAAATGATGC 184
 Qy 3365 TATGCTTAGATTAGGGGTTTTCGAACTGAGGCTTATAACAAAGTCTTCTCGGAAGTAA 3424
 Db 185 TATGCTTAGATTAGGGGTTTTCGAACTGAGGCTTATAACAAAGTCTTCTCGGAAGTAA 244
 Qy 3425 TTGTAGCATCTCGAAATAAAGACGAAATATGAAAGATAGTTGAGACTGTTAATATAC 3484
 Db 245 TTGTAGCATCTCGAAATAAAGACGAAATATGAAAGATAGTTGAGACTGTTAATATAC 304
 Qy 3485 AGATTCTCTCCATATCTGATTTTCAGATACTTAGAACACGCTATGCGAAGTAGTCATGC 3544
 Db 305 AGATTCTCTCCATATCTGATTTTCAGATACTTAGAACACGCTATGCGAAGTAGTCATGC 364
 Qy 3545 ATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGTTGTAATAAGGAAGA 3604
 Db 365 ATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGTTGTAATAAGGAAGA 424
 Qy 3605 TACTAGTTTGTCTGAAATGACATTTAGGAAAGTCTGCTGTTTGTAGCAAAAGCGTCCA 3664
 Db 425 TACTAGTTTGTCTGAAATGACATTTAGGAAAGTCTGCTGTTTGTAGCAAAAGCGTCCA 484
 Qy 3665 GAGAGGAGAGCTTAGCAGGAGTCTCTAGCCCTTTTCCACCCATACACATTTGGCTCAGGTTA 3724
 Db 485 GAGAGGAGAGCTTAGCAGGAGTCTCTAGCCCTTTTCCACCCATACACATTTGGCTCAGGTTA 544
 Qy 3725 CCGAAGAGGCGCCAGAAATTAGAGTCTCTCAGAGAGAACTTATCTAGTGAGGATGAAGA 3784
 Db 545 CCGAAGAGGCGCCAGAAATTAGAGTCTCTCAGAGAGAACTTATCTAGTGAGGATGAAGA 604
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 Qy 3845 TAGGCATAGCACCGTCTCAGGAGTCTGCTGTAGAAACACAGAGAGATTTATTATTC 3904
 Db 565 TAGGCATAGCACCGTCTCAGGAGTCTGCTGTAGAAACACAGAGAGATTTATTATTC 724
 Qy 3905 ATTGAGAGATAGCTTTAAATGACTGAGTAAACCGAGGTAATATTGGCAAG 3953
 Db 725 ATTGAGAGATAGCTTTAAATGACTGAGTAAACCGAGGTAATATTGGCAAG 772

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LOCUS      BUI71200
DEFINITION AGENCOURT_7956206 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6161612
5', mRNA sequence.
ACCESSION  BUI71200
VERSION    BUI71200.1 GI:22685184
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 933)
            NIH-MGC http://mgs.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTF
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LHAM1514 row: c column: 21
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                /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
                Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                Average insert size 2 kb. Library constructed by Life
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ORIGIN
Query Match      13.1%; Score 746.4; DB 13; Length 933;
Best Local Similarity 98.3%; Pred. No. 6.5e-159;
Matches 765; Conservative 0; Mismatches 11; Indels 2; Gaps 1;
QY 4709 GGTGTTGATGTGGAGGACACAGCTGGAGAGTCTGGGCCACACGATTTGACGGAAC 4768
DB 12 GGTGTTGATGTGGAGGACACAGCTGGAGAGTCTGGGCCACACGATTTGACGGAAC 71
QY 4769 ATCTTACTTGCACGGCAAGATCTAGAGGGAACCCCTTACCTGGAATCTGGAATCAGCCT 4828
DB 72 ATCTTACTTGCACGGCAAGATCTAGAGGGAACCCCTTACCTGGAATCTGGAATCAGCCT 131
QY 4829 CTCTCTGATGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4888
DB 132 CTCTCTGATGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 191
QY 4889 TGGCAACATACATCTTCAACTCTGCATTGGAAGTCCCAATTTGAAAGTTGCAAGATC 4948
DB 192 TGGCAACATACATCTTCAACTCTGCATTGGAAGTCCCAATTTGAAAGTTGCAAGATC 251
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DB 252 TGCCAGGGTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 311
QY 5009 AAGTGTGACGGGAGAGCCAGATTCAGAGCTTCAACAGAAAGGGTCAACAAAGAT 5068
DB 312 AAGTGTGACGGGAGAGCCAGATTCAGAGCTTCAACAGAAAGGGTCAACAAAGAT 371
QY 5069 GTCCATGTGTGTCTGGCCTGACCCAGAGAAATTTATGCTGTGTACAAAGTTTGCCAG 5128
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QY 5249 AAAATGGTGTAGTGTATTTCTGGGTGACCCAGTCTATTAAAGAAAGAAAATGCTGAA 5308
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DB 612 TGAGCATGATTTTGAAGTCAGAGAGATGTGGTCAATGGAAGAAACACCAAGGTCCAAA 671
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DB 672 GCGAGCBAAGAGATCCCGAGCAGAGATCTTCAGGGGGCTAGAAATCTGTGCTATGG 731
QY 5429 GCCCTTCCACACATGCCACAG--ATCAACTGGAATGGATGGTACAGCTGTGTGGTG 5484
DB 732 GCCCTTCCACACATGCCACAGNNATCACTGGGAATGGATGGGTACAGCTGTGGTG 789

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LOCUS      BG681276
DEFINITION 602627125F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4751887 5',
mRNA sequence.
ACCESSION  BG681276
VERSION    BG681276.1 GI:13912673
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            1 (bases 1 to 743)
            NIH-MGC http://mgs.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LHAM10609 row: a column: 08
            High quality sequence stop: 741.
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                Average insert size 1.5kb. Library constructed by Life
                Technologies. Note: this is a NCI CGAP Library."
ORIGIN
Query Match      12.9%; Score 738.8; DB 12; Length 743;
Best Local Similarity 99.7%; Pred. No. 3.3e-157;
Matches 740; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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 1 GGAGCAACAGCTGGAGAGCTCTGGSCACACGATTGACGAAAATCTTACTTCCCAAG 60
 4784 GCAAGATCTAGAGGGAACCCCTTACTTGGAAATCTGGAATCAGCCCTCTTCTCTGATGACCC 4843
 61 GCAAGATCTAGAGGGAACCCCTTACTTGGAAATCTGGAATCAGCCCTCTTCTCTGATGACCC 120
 4844 TGAATCTGATCTCTCTGAGACAGAGCCGCCAGAGTCTGCTGTTGGCAACATACCATC 4903
 121 TGAATCTGATCTCTCTGAGACAGAGCCGCCAGAGTCTGCTGTTGGCAACATACCATC 180
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 5264 CTATTTCTGGTGACCCAGCTCTATTAAAGAAAGAAATGCTGAATGAGCATGTTTGA 5323
 541 CTATTTCTGGTGACCCAGCTCTATTAAAGAAAGAAATGCTGAATGAGCATGTTTGA 600
 5324 AGTCAGAGAGATGTGGTCAATGGAAGAAACCAACCAAGTCCAAAGCGAGCAAGAAATC 5383
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 5384 CCAGGACAGAAAGATCTTCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCACCAAT 5443
 661 CCAGGACAGAAAGATCTTCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCACCAAT 720
 5444 GCCACAGATCAACTGGAATGG 5465
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RESULT 12
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 5' mRNA sequence.

ACCESSION BQ422380
 VERSION BQ422380.1 GI:21117695
 KEYWORDS EST.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens (human)

REFERENCE
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 CONTACT Contact: Robert Strausberg, Ph.D.
 EMAIL Email: cgabbs-r@mail.nih.gov
 TISSUE Tissue Procurement: ATCC

cdna Library Preparation: life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLAM13280 row: n column: 05
 High quality sequence stop: 597.

FEATURES

Location/Qualifiers
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 /tissue type="embryonal carcinoma, cell line"
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 /clone lib="NIH_MGC_92"
 /note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 2.5 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 12.9% Score 734.6; DB 13; Length 899;
 Best Local Similarity 97.1%; Pred. No. 3.1e-156;
 Matches 824; Conservative 0; Mismatches 11; Indels 14; Gaps 7;
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 DB 16 CAGGCTGTGGGTTTCTCAGATAA CTGGGCCCTCGCCTCAGGAGGCTTCACCTCTGC 75
 QY 90 TCTGGGTAAAGTTCAATTTGGACAGAAAGAAATGATTTATCTGCTTCGCGTTGAAGAA 149
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 QY 150 GTACAAATGTCTAATATGCTATGTCAGAAAATCTTAGAGTGTCCTATCTGTCTGAGTTG 209
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 QY 210 ATCAAGAACTGTCTCCACAAAGTGTGACCAATATTTGCAATTTTGCATCTGCTGAAA 269
 DB 190 ATCAAGAACTGTCTCCACAAAGTGTGACCAATATTTGCAATTTTGCATCTGCTGAAA 249
 QY 270 CTCTCAACAGAGAAAGGCTTCACAGTGTCTCTTATGTAAGAAATGATATACCAAA 329
 DB 250 CTCTCAACAGAGAAAGGCTTCACAGTGTCTCTTATGTAAGAAATGATATACCAAA 309
 QY 330 AGGAGCTTACAGAAAGTACAGATTTAGTCACTTGTGAGAGCTATTGAAAATCATTT 389
 DB 310 AGGAGCTTACAGAAAGTACAGATTTAGTCACTTGTGAGAGCTATTGAAAATCATTT 369
 QY 390 TGTGCTTTTTCAGCTTGTGACAGAGTTTTCAGATGTATGCAACAGCTATAATTTTGCAAAAG 449
 DB 370 TGTGCTTTTTCAGCTTGTGACAGAGTTTTCAGATGTATGCAACAGCTATAATTTTGCAAAAG 429
 QY 450 GAAATAAATCTCTCTGAACATCTAAAAGATGAAGTTTCTATCATCCAAAGATGGCTAC 509
 DB 430 GAAATAAATCTCTCTGAACATCTAAAAGATGAAGTTTCTATCATCCAAAGATGGCTAC 489
 QY 510 AGAAACCTGTCGCAAAAGACTTCTACAGAGTGAACCCGAAATCTCTTCCCTTCAGAGAAACC 569
 DB 490 AGAAACCTGTCGCAAAAGACTTCTACAGAGTGAACCCGAAATCTCTTCCCTT---GGAACCC 546
 QY 570 AGTCTCAGTGTCCAACTCTCTTAACCTTGGAACTGTGAGAACTCTGAGGACAAAGACGG 629
 DB 547 AGTCTCAGTGTCCAACTCTCTTAACCTTGGAACTGTGAGAACTCTGAGGACAAAGACGG 606
 QY 630 ATACAACCTCAAAAGAGCTCTGTGATGAAATGGATGCTGATTTCTTCTGAGATACC 689
 DB 607 ATACAACCTCAAAAGAGCTCTGTGATGAAATGGATGCTGATTTCTTCTGAGATACC 666
 QY 690 GTTAATAAGGCAACTTATTTCAGTGCTGGAGATCAAGAAATGTTTACAAATCACCCTCAA 749


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Db      667 GTTAAAGGCACTTATTGAGTGTGGAGATCAGANTTGTACAAATCAACCCCTCA 726
Qy      750 GGAACCA-GGGATGAATCAGTTGGATTCTGCAAAAAGCGTGC-TTGGAATTTCTG 807
Db      727 GGAACCAAGGATGAATCAGTTGGATTCTGCAAAAAGCGTGC-TTGGAATTTCTG 786
Qy      808 AGACGGATGAACA-ATACCTGACATC-ATCAACCCAGTAATAATGA-TTGAACACCA 864
Db      787 AGACGGATGTACAANATCTGACATCAATCAACCCAGTAATAATGTTTGAACACCA 846
Qy      865 CTGAGAGC 873
Db      847 CTGGAAC 855

RESULT 13
BO215100 878 bp mRNA linear EST 02-MAY-2002
AGENCOURT 7591049 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6065516
5', mRNA sequence.
ACCESSION BO215100
VERSION BO215100.1 GI:20396500
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 878)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTb/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13341 row: 0 column: 21
High quality sequence stop: 669.
FEATURES
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:6065516"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN
Query Match 12.4%; Score 706.2; DB 13; Length 878;
Best Local Similarity 98.8%; Pred. No. 9.2e-150;
Matches 754; Conservative 0; Mismatches 3; Indels 6; Gaps 4;

Qy      30 CAGCTGTGGGTTTCTCAGATACTGGCCCTCGGCTCAGGAGGCTTCAACCTCTGC 89
Db      13 CAGCTGTGGGTTTCTCAGATACTGGCCCTCGGCTCAGGAGGCTTCAACCTCTGC 72
Qy      90 TCTGGGTAAGTTCATTGGACACAGAAAGAAATGATTATCTGCTTCGGTTGAAGAA 149
Db      73 TCTGGGTAAGTTCATTGGACACAGAAAGAAATGATTATCTGCTTCGGTTGAAGAA 132
Qy      150 GTACAAATGTCATTAATGCTATCGCAAAATCTTAGAGTCCCATCTGCTCGAGTTG 209
Db      133 GTACAAATGTCATTAATGCTATCGCAAAATCTTAGAGTCCCATCTGCTCGAGTTG 192

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Qy      210 ATCAGGACCTGTCTCCACAAAGTGTGACCATATTTTGCATAATTTTCATGCTGAAA 269
Db      193 ATCAGGAACTGTCTCCACAAAGTGTGACCATATTTTGCATAATTTTCATGCTGAAA 252
Qy      270 CTTCTCAACAGAGAAAGGGCTTTCACAGTGTCTCTTTATGTAAGAAATGATTAACAAA 329
Db      253 CTTCTCAACAGAGAAAGGGCTTTCACAGTGTCTCTTTATGTAAGAAATGATTAACAAA 312
Qy      330 AGAGGCTTACAGAAAGTACGAGATTAGTCAACTGTTGAGAGCTATTGAAAATCATTT 389
Db      313 AGAGGCTTACAGAAAGTACGAGATTAGTCAACTGTTGAGAGCTATTGAAAATCATTT 372
Qy      390 TGTGCTTTTTCAGCTTGACACAGCTTTGGAGTAGTGCACACAGCTATAATTTTGCAAAAAG 449
Db      373 TGTGCTTTTTCAGCTTGACACAGCTTTGGAGTAGTGCACACAGCTATAATTTTGCAAAAAG 432
Qy      450 GAAATATCTCTCTGAACTCTAAAGATGAAGTTTCTATCATCCAAAGTAGTGGCTAC 509
Db      433 GAAATATCTCTCTGAACTCTAAAGATGAAGTTTCTATCATCCAAAGTAGTGGCTAC 492
Qy      510 AGAAACCGTGCACAAAGACTTCTACAGAGTGAACCCGAAATCTCTTCCTTGCAGGAAAC 569
Db      493 AGAAACCGTGCACAAAGACTTCTACAGAGTGAACCCGAAATCTCTTCCTTGCAGGAAAC 549
Qy      570 AGTTCAGTGTCAACTCTCTTAACCTTGAACCTGTGAGAACTCTGAGGACAAAGCAGCG 629
Db      550 AGTTCAGTGTCAACTCTCTTAACCTTGAACCTGTGAGAACTCTGAGGACAAAGCAGCG 609
Qy      630 ATACACCTCAAAAGAGCTGTCTACATTGAATTTGGAGTCTGATTTCTTCTGAGATACC 689
Db      610 ATACACCTCAAAAGAGCTGTCTACATTGAATTTGGAGTCTGATTTCTTCTGAGATACC 669
Qy      690 GTTAATAAGCCAACTTATTGCACT-GTGGAGATCAAGAAATGTTTCAAAATCACCCCTCA 748
Db      670 GTTAATAAGCCAACTTATTGCACTGTGGAGATCAAGAAATGTTTCAAAATCACCCCTCA 729
Qy      749 AGGAACCA-GGATGAAATCAG-TTGGATCTTGCAGAAAGS 789
Db      730 AGGACCAAGGATGAATCACTGTTTGGATCTTGCAGAAAGS 772

RESULT 14
CF121736 739 bp mRNA linear EST 09-SEP-2003
LOCUS UI-RP-BPop-arn-g-04-0-UI.r1 NIH_MGC_51 Homo sapiens cDNA clone
DEFINITION IMAGE:30566859 5', mRNA sequence.
ACCESSION CF121736
VERSION CF121736
KEYWORDS CF121736.1 GI:33194237
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 739)
AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.
TITLES Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEERF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Louis Staudt
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at

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http://genome.uiowa.edu/distribution/humanfl.html
Seq primer: pYX-5.

FEATURES

Location/Qualifiers

1..739

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/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH MGC 51"
/note="Vector: pYX3-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(4.4-7.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 12.3%; Score 701.2; DB 14; Length 739;
Best Local Similarity 98.0%; Pred. No. 1.2e-148;
Matches 720; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

QY 2352 GAAGACCCCAAGATCTCATGTTAGTGGAGAGGGTTTCGAACTGGAAGATCTGTA 2411
DB 6 GGAGACCCCAAGATCTCATGTTANAGTGGAGAGGGTTTCGAACTGGAAG-TCGTGA 64

QY 2412 GAGAGTAGCAGTATTTCACTGGTACTGCTACTGATTTATGGCACTCAGGAAAGTATCTCG 2471
DB 65 GAGAGTAGCAGTATTTCACTGGTACTGCTACTGATTTATGGCACTCAGGAAAGTATCTCG 124

QY 2472 TTACTGGAGTTAGCACTCTAGGAGGCAAAACAGAACCAATAATGTTGAGTCAAG 2531
DB 125 TTACTGGAGTTAGCACTCTAGGAGGCAAAACAGAACCAATAATGTTGAGTCAAG 184

QY 2532 TGTCAGAGTATTTGAAACCCCAAGGCACTAATTTCACTGTTGTTCCAAAGATAATAGAAAT 2591
DB 185 TGTCAGAGTATTTGAAACCCCAAGGCACTAATTTCACTGTTGTTCCAAAGATAATAGAAAT 244

QY 2592 GACACAGAGGCTTTAAGTATCCATTTGGGACATGAAGTTAACCAAGTCGGGAAACAAGC 2651
DB 245 GACACAGAGGCTTTAAGTATCCATTTGGGACATGAAGTTAACCAAGTCGGGAAACAAGC 304

QY 2652 ATAGAAATGGAAGAAAGTGAACCTTCATGCTCAGTATTTGCAGATACATTTCAAGTTTCA 2711
DB 305 ATAGAAATGGAAGAAAGTGAACCTTCATGCTCAGTATTTGCAGATACATTTCAAGTTTCA 364

QY 2712 AAGGCCAGTCAATTTGCTCTGTTTTCAAATCAGGAATGCAAGAAATGCAAGAGAAATGTCACAA 2771
DB 365 AAGGCCAGTCAATTTGCTCTGTTTTCAAATCAGGAATGCAAGAAATGCAAGAGAAATGTCACAA 424

QY 2772 TTCTGCGCCACTCTGGGTCCTTAAGAAACAAAGTCCAAAGTCACTTTTGAATGTGA 2831
DB 425 TTCTGCGCCACTCTGGGTCCTTAAGAAACAAAGTCCAAAGTCACTTTTGAATGTGA 484

QY 2832 CAAAGGAGAGAAATCAAGGAAAGAAATGAGTCTAATATCAAGCCCTGTACAGACAGTTAAT 2891
DB 485 CAAAGGAGAGAAATCAAGGAAAGAAATGAGTCTAATATCAAGCCCTGTACAGACAGTTAAT 544

QY 2892 ATCACTGAGGCTTTCCTGTTGGTTCAGAAAGTAAGCAAGTGTATGATGCCAATGT 2951
DB 545 ATCACTGAGGCTTTCCTGTTGGTTCAGAAAGTAAGCAAGTGTATGATGCCAATGT 604

QY 2952 AGTATCAAGGAGGCTTTCCTGTTGGTTCATCATCTCAGTTTCAGAGGCAACGAACTGGA 3011
DB 605 AGTATCAAGGAGGCTTTCCTGTTGGTTCATCATCTCAGTTTCAGAGGCAACGAACTGGA 664

QY 3012 CTCATTACTCCAAATAACATGGACTTTTACAAACCCATATGCTATACCAACCACTTTT 3071
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QY 3072 CCCATCAAGTCAATTT 3086

Db 725 TCCATCAAGTCAATTT 739

RESULT 15

BUI47444

LOCUS

DEFINITION

BUI47444

ACCESSION

BUI47444

VERSION

BUI47444.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 856)

AUTHORS

NIH-MGC http://mgs.nci.nih.gov/

JOURNAL

National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: Dr. James R. Lupski

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LUAM13566 row: 0 column: 13

High quality sequence stop: 695.

FEATURES

Location/Qualifiers

1..856

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/clone="IMAGE:6181860"

/sex="male"

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/dev_stage="adult, 36 yr"

/lab_host="DH10B"

/clone_lib="Lupski dorsal root ganglion"

/notes="Vector: pCMV-SPORT6 (Life Technologies); Site 1:

NotI; Site 2: SalI; cDNA made by oligo-dT priming.

Directionally cloned using the following adaptors:

5'-TCGACCCAGGCTCCG-3' and

5'-GACTAGTCTAGATCGGACGCGCCCT(15)-3'. Size selected >

1 Kb for average insert length 1.7 Kb. This is a primary

library, non-amplified. Library constructed by Life

Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor

College of Medicine) and is available through Life

Technologies."

ORIGIN

Query Match 12.2%; Score 698; DB 13; Length 856;

Best Local Similarity 97.9%; Pred. No. 6.7e-148;

Matches 762; Conservative 0; Mismatches 5; Indels 11; Gaps 5;

QY 1 AGCTCGCTGAGACTTCCTGGAGCCGCCAGCCAGGCTGTGGGGTTCTCAGATAACTGGGCC 60

DB 82 AGCTCGCTGAGACTTCCTGGAGCCGGGGA-CAGGCTGTGGGGTTCTCAGATAACTGGGCC 140

QY 61 CCTGCGCTCAGGAGGCTTCACCCCTCTGCTCTGGTAAAGTTCAATTCGAAACAGAAAGAAA 120

DB 141 CCTGCGCTCAGGAGGCTTCACCCCTCTGCTCTG-----GTTCAATTCGAAACAGAAAGAAA 194

QY 121 TGGATTTATCTCTCTTCGGGTTGAGAGAGTACAAATGTCATTAATGCTATCGAGAAA 180

DB 195 TGGATTTATCTCTCTTCGGGTTGAGAGAGTACAAATGTCATTAATGCTATCGAGAAA 254

QY 181 TCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGGAACCTGCTCCACAAAGTGTGACC 240

DB 255 TCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGGAACCTGCTCCACAAAGTGTGACC 314

Qy	241	ACATATTTTGCATTTTGCATGCTGAAACTTCTCAACCAAGAAAGGGCCTTTCACAGT	300
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Qy	301	GTCCTTTATGTAAGTAATGATATATACCAAAAGAGGCTTACAAGAAAGTACGAGATTTAGTC	360
Db	375	GTCCTTTATGTAAGTAATGATATATACCAAAAGAGGCTTACAAGAAAGTACGAGATTTAGTC	434
Qy	361	AACTTGTGTAAGAGCTATTGAAATCAATTTGTGCTTTTTCAGCTTGACACAGGTTTGGAGT	420
Db	435	AACTTGTGTAAGAGCTATTGAAATCAATTTGTGCTTTTTCAGCTTGACACAGGTTTGGAGT	494
Qy	421	ATGCAACAGCTATAATTTTGCAGAAAGGAAATTAATCTCTCTGAAATCTTAAAGATG	480
Db	495	ATGCAACAGCTATAATTTTGCAGAAAGGAAATTAATCTCTCTGAAATCTTAAAGATG	554
Qy	481	AACTTGTGTAAGAGCTATTGAAATCAATTTGTGCTTTTTCAGCTTGACACAGGTTTGGAGT	540
Db	555	AACTTGTGTAAGAGCTATTGAAATCAATTTGTGCTTTTTCAGCTTGACACAGGTTTGGAGT	614
Qy	541	AACTTGTGTAAGAGCTATTGAAATCAATTTGTGCTTTTTCAGCTTGACACAGGTTTGGAGT	600
Db	615	AACTTGTGTAAGAGCTATTGAAATCAATTTGTGCTTTTTCAGCTTGACACAGGTTTGGAGT	674
Qy	601	CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTTCAAGACCTCTGTCTACATG	660
Db	675	CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTTCAAGACCTCTGTCTACATG	734
Qy	661	AATTGGGATCTGATCTTCTGAGATACCGTTTAAAGGCAACTTATTGCAAGTGTGNGA	719
Db	735	AATTGGGATCTGATCTTCTGAGATACCGTTTAAAGGCAACTTATTGCAAGTGTGNGA	794
Qy	720	GATCAAG-AATTGTTACAAATCAACCCCTCAAGGACCAAGG--ATGAATCAGTTTG	774
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Search completed: June 12, 2004, 06:28:03
Job time : 13209 secs

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US-08-798-691-5									
Query Match 100.0%; Score 5711; DB 1; Length 5711;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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QY	61	CTGCGCTCAGAGGCTTCACTCTGCTGCTGGTAAAGTTCATTTGGACAGAGAA	120						
DB	61	CTGCGCTCAGAGGCTTCACTCTGCTGCTGGTAAAGTTCATTTGGACAGAGAA	120						
QY	121	FGGATTTATCTGCTCTCTGCGTTTGAAGAAGTACAAAATGTCATTAATGCTATGCGAGAA	180						
DB	121	TGGATTTATCTGCTCTCTGCGTTTGAAGAAGTACAAAATGTCATTAATGCTATGCGAGAA	180						
QY	181	TCTAGAGTGTCCATCTGTCTGGAGTTGATCAGGAACTGTCTCCACAAAGTGTGACC	240						
DB	181	TCTAGAGTGTCCATCTGTCTGGAGTTGATCAGGAACTGTCTCTCCACAAAGTGTGACC	240						
QY	241	ACATATTTGCAAAATTTGCACTGCTGAACTTCTCAACAGAGAGAGGCGCTTCACT	300						
DB	241	ACATATTTGCAAAATTTGCACTGCTGAACTTCTCAACAGAGAGAGGCGCTTCACT	300						
QY	301	GTCTTTATGAGATGATATACCAAGAGGCTTACAGAAAGTACGAGATTTAGTC	360						
DB	301	GTCTTTATGAGATGATATACCAAGAGGCTTACAGAAAGTACGAGATTTAGTC	360						
QY	361	AACCTTTGAGAGCTATTTGCAAAATGATTTGCTCTTTCAGCTTGACACAGGTTTGGAGT	420						
DB	361	AACCTTTGAGAGCTATTTGCAAAATGATTTGCTCTTTCAGCTTGACACAGGTTTGGAGT	420						
QY	421	ATGCAAAACAGCTATAATTTTGCAGAAAGGAAATTAACCTCTCTGCAACATCTAAAGATG	480						
DB	421	ATGCAAAACAGCTATAATTTTGCAGAAAGGAAATTAACCTCTCTGCAACATCTAAAGATG	480						
QY	481	AAGTTTCTATCATCCAAAGTATGGCTACAGAAACGTCGCCAAGAGACTTCTACAGAGTG	540						
DB	481	AAGTTTCTATCATCCAAAGTATGGCTACAGAAACGTCGCCAAGAGACTTCTACAGAGTG	540						
QY	541	AACCCGAAATCTCTCTGAGGAAACAGCTCTCAGTGTCCAACTCTCTAAGCTTTGGAA	600						
DB	541	AACCCGAAATCTCTCTGAGGAAACAGCTCTCAGTGTCCAACTCTCTAAGCTTTGGAA	600						
QY	601	CTGTGAGACTCTGAGGACAAAGCAGCGGATACAACTCAGGAGCTCTGTCTACATTTG	660						
DB	601	CTGTGAGACTCTGAGGACAAAGCAGCGGATACAACTCAGGAGCTCTGTCTACATTTG	660						
QY	661	AATTTGGATCTGATTTCTTGAAGATACCGTTAATAGGCACTTATTTGAGTGTGGAG	720						
DB	661	AATTTGGATCTGATTTCTTGAAGATACCGTTAATAGGCACTTATTTGAGTGTGGAG	720						
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DB	781	CABAAAGGCTGTGTGTAATTTCTGAGACGAGTGTACAAATCTGAGCATCATCAAC	840						
QY	841	CCAGTATATGATTTTGAACCACTGAGAGCGTGCAGCTGAGAGGCTATCCAGAAAGT	900						
DB	841	CCAGTATATGATTTTGAACCACTGAGAGCGTGCAGCTGAGAGGCTATCCAGAAAGT	900						
QY	901	ATCAGGATGTTCTGTTGAACTTTCAGATGTGAGGCAATGTGCAAAATCTCATGCCA	960						
DB	901	ATCAGGATGTTCTGTTGAACTTTCAGATGTGAGGCAATGTGCAAAATCTCATGCCA	960						
QY	961	GCTCATTACAGCTGAGAGCAGGTTTATTTACTCACTAAGACAGATGAAATGTAGAAA	1020						
DB	961	GCTCATTACAGCTGAGAGCAGGTTTATTTACTCACTAAGACAGATGAAATGTAGAAA	1020						

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 11, 2004, 20:16:35 ; Search time 356 Seconds
(without alignments)
8902.597 Million cell updates/sec

Title: US-09-734-672A-3
Perfect score: 5711
Sequence: 1 ACCTGCTCAGACTTCCTGG.....TCCCCCAGCCACTACTGA 5711

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 segs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
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4: /cgn2.6/prodata/2/ina/6B COMB.seq: *
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6: /cgn2.6/prodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	5711	100.0	5711	3 US-08-825-886-10	Sequence 5, Appli
3	5711	100.0	5711	3 US-09-074-476-3	Sequence 3, Appli
4	5709.4	100.0	5711	1 US-08-598-591-1	Sequence 1, Appli
5	5709.4	100.0	5711	1 US-08-798-691-1	Sequence 1, Appli
6	5709.4	100.0	5711	3 US-08-825-886-1	Sequence 1, Appli
7	5709.4	100.0	5711	3 US-09-074-476-1	Sequence 1, Appli
8	5707.8	99.9	5711	4 US-10-022-819-1	Sequence 1, Appli
9	5703	99.9	5711	1 US-08-798-691-3	Sequence 3, Appli
10	5703	99.9	5711	3 US-08-825-886-3	Sequence 3, Appli
11	5703	99.9	5711	3 US-09-074-476-5	Sequence 5, Appli
12	5701.4	99.8	5711	2 US-08-658-322-1	Sequence 1, Appli
13	5701.4	99.8	5712	2 US-08-603-753D-1	Sequence 1, Appli
14	5701.4	99.8	5712	3 US-09-099-753-1	Sequence 1, Appli
15	5701.4	99.8	5712	3 US-08-986-106-1	Sequence 1, Appli
16	5701.4	99.8	5712	4 US-09-007-678B-47	Sequence 47, Appli
17	5701.4	99.8	5714	1 US-08-480-784-1	Sequence 1, Appli
18	5701.4	99.8	5714	1 US-08-483-553-1	Sequence 1, Appli
19	5701.4	99.8	5714	1 US-08-487-002-1	Sequence 1, Appli
20	5701.4	99.8	5714	1 US-08-483-554B-1	Sequence 1, Appli
21	5701.4	99.8	5714	1 US-08-488-011B-1	Sequence 1, Appli
22	5701.4	99.8	5714	1 US-08-850-727-1	Sequence 1, Appli
23	5701.4	99.8	5714	5 PCT-US95-10202-1	Sequence 1, Appli
24	5701.4	99.8	5714	5 PCT-US95-10203-1	Sequence 1, Appli
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31 5699.8 99.8 5711 4 US-08-989-890-10 Sequence 10, Appli
32 5690.4 99.6 5712 1 US-08-425-061-12 Sequence 12, Appli
33 5690.4 99.6 5712 1 US-08-825-886-12 Sequence 12, Appli
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43 5687.4 99.6 5709 1 US-08-825-886-7 Sequence 7, Appli
44 5687.4 99.6 5709 1 US-08-825-886-8 Sequence 8, Appli
45 5687.4 99.6 5709 1 US-08-825-886-9 Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-08-798-691-5
; Sequence 5, Application US/08798691
; Patent No. 5750400
; GENERAL INFORMATION:
; APPLICANT: Murphy, Patricia D.
; APPLICANT: Aliens, Antonette C.
; APPLICANT: Alvares, Christopher P.
; APPLICANT: Critz, Brenda S.
; APPLICANT: Olson, Sheri J.
; APPLICANT: Schelter, Denise B.
; APPLICANT: Zeng, Bin
; TITLE OF INVENTION: Coding Sequences of the Human
; TITLE OF INVENTION: BRCA1 Gene
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ONCORMED
; CITY: Gaithersburg
; STREET: 200 Perry Parkway
; STATE: MD
; COUNTRY: USA
; ZIP: 20877

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798.691
; FILING DATE: 12-Feb-97
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas Gallegos
; REGISTRATION NUMBER: 32,692
; REFERENCE/DOCKET NUMBER: PA-0054CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-527-2051
; TELEFAX: 301-208-6997
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; STRAIN: BRCA1
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 17

QY 241 ACATATTTTGCATTTTTCATGCTGCTGAACTTTCTCAACACAGAGAGAGGCGCTTTCACAGT 300
Db |||||||
QY 315 ACATATTTTTCGAAATTTTTCATGCTGCTGAACTTTCTCAACACAGAGAGAGGCGCTTTCACAGT 374
Db |||||||
QY 301 GTCCTTTATGTAGAATGATATATACCAAAAGGAGCCTTACAGAAAGTACAGATTTTAGTC 360
Db |||||||
QY 375 GTCCTTTATGTAGAATGATATATACCAAAAGGAGCCTTACAGAAAGTACAGATTTTAGTC 434
Db |||||||
QY 361 AACTTGTGTGAGAGCTATTGAATCATTTTGTGCTTTTTCAGCTTTGACACAGGTTTGGAGT 420
Db |||||||
QY 435 AACTTGTGTGAGAGCTATTGAATCATTTTGTGCTTTTTCAGCTTTGACACAGGTTTGGAGT 494
Db |||||||
QY 421 ATGCAACACAGCTATAATTTTTCGAAAAAGGAAAAATAACTCTCTCTGAAACATCTAAAAAGATG 480
Db |||||||
QY 495 ATGCAACACAGCTATAATTTTTCGAAAAAGGAAAAATAACTCTCTCTGAAACATCTAAAAAGATG 554
Db |||||||
QY 481 AAGTTTCTATCATTCRAAGTATGGCTACAGAAACCGTGCRAAGAGACTTCTACAGAGTG 540
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QY 555 AAGTTTCTATCATTCRAAGTATGGCTACAGAAACCGTGCRAAGAGACTTCTACAGAGTG 614
Db |||||||
QY 541 AACCCGAAAAATCCTTCTGAGGAAACCACTCTCAGTGTCCAACTCTCTAACCTTGGAA 600
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QY 615 AACCCGAAAAATCCTTCTGAGGAAACCACTCTCAGTGTCCAACTCTCTAACCTTGGAA 674
Db |||||||
QY 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCTCAAGAGACGCTCTGTCTACATTG 660
Db |||||||
QY 675 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCTCAAGAGACGCTCTGTCTACATTG 734
Db |||||||
QY 661 AATTGGGATCTGATTCTTCTGAGATACCGTTAATAAGGCAACTTATTGCAAGTG- GGA 719
Db |||||||
QY 735 AATTGGGATCTGATTCTTCTGAGATACCGTTAATAAGGCAACTTATTGCAAGTG- GGA 794
Db |||||||
QY 720 GATCAAG- AATTGTTACAAATCACCCCTCAAGGAAACCAAGG- -ATGAAATCAGTTTGG 774
Db |||||||
QY 795 GATCAGAAATTTGTTACAAATCACCCCTCAAGGAAACCAAGGAAATGAATCAGTTTGG 852
Db |||||||

Search completed: June 12, 2004, 06:28:03
Job time : 13209 secs

POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
US-08-823-487A-5

Query Match 100.0%; Score 5711; DB 3; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AGCTCGCTCAGACTTCTCGACCCCGCCACCGGCTGTGGGGTTCTCAGATAACTGGGCC	60
DB	1	AGCTCGCTCAGACTTCTCGACCCCGCCACCGGCTGTGGGGTTCTCAGATAACTGGGCC	60
QY	61	CTGGGCTCAGAGGCTTCAACCTCTGCTCTGGGTAAAGTTCTTGGACAGAAAGAAA	120
DB	61	CTGGGCTCAGAGGCTTCAACCTCTGCTCTGGGTAAAGTTCTTGGACAGAAAGAAA	120
QY	121	TGGATTATCTGCTCTTCCGCTTGAAGAGTACAAAATGTCATTAATGCTATGCAGAAAA	180
DB	121	TGGATTATCTGCTCTTCCGCTTGAAGAGTACAAAATGTCATTAATGCTATGCAGAAAA	180
QY	181	TCCTAGAGTCCCATCTGCTGAGGTTGATCAGAGAACCTGCTCCACAAAGTGTGACC	240
DB	181	TCCTAGAGTCCCATCTGCTGAGGTTGATCAGAGAACCTGCTCCACAAAGTGTGACC	240
QY	241	ACATATTTGCAAAATTTTCATGCTGAAACTTCTCAACAGAGAAAGGGCTTCCACAGT	300
DB	241	ACATATTTGCAAAATTTTCATGCTGAAACTTCTCAACAGAGAAAGGGCTTCCACAGT	300
QY	301	GTCCCTTTATGTAAGATGATATAACCAAAAGAGGCTTACAGAAAGTACGAGATTAGTC	360
DB	301	GTCCCTTTATGTAAGATGATATAACCAAAAGAGGCTTACAGAAAGTACGAGATTAGTC	360
QY	361	AACTGTTGCAAGCTTATGAAATCATTTGCTTTTTCAGCTTCGACACAGGTTTGGAGT	420
DB	361	AACTGTTGCAAGCTTATGAAATCATTTGCTTTTTCAGCTTCGACACAGGTTTGGAGT	420
QY	421	ATGCAAAACAGCTATTAATTTTGCAAAAGGAAATAAATCTCTCGAAATCTTAAAGATG	480
DB	421	ATGCAAAACAGCTATTAATTTTGCAAAAGGAAATAAATCTCTCGAAATCTTAAAGATG	480
QY	481	AACTTTCTATCATCCAAAGTATGGCTACAGAAACGGTCCAAAGAGCTTCTACAGAGTG	540
DB	481	AACTTTCTATCATCCAAAGTATGGCTACAGAAACGGTCCAAAGAGCTTCTACAGAGTG	540
QY	541	AAACCGAATCTCTCTTTCAGGAAACAGTCTCAGTGTCCAACTCTCTAACCTTTGAA	600
DB	541	AAACCGAATCTCTCTTTCAGGAAACAGTCTCAGTGTCCAACTCTCTAACCTTTGAA	600
QY	601	CTGTGAGAACTCTGAGGACAAAGCAGCGGATCAACCTCAAAAGAGCTCTGTCTCATTTG	660
DB	601	CTGTGAGAACTCTGAGGACAAAGCAGCGGATCAACCTCAAAAGAGCTCTGTCTCATTTG	660
QY	661	AATTGGGATCTGATTTCTGAGATACCGTTTAAATAGGCACTTATTGCACTGGGAG	720
DB	661	AATTGGGATCTGATTTCTGAGATACCGTTTAAATAGGCACTTATTGCACTGGGAG	720
QY	721	ATCAGAAATTTGTAACAAATCACCCCTCAAGGAAACAGGATGAATTCAGTTTGGATCTG	780
DB	721	ATCAGAAATTTGTAACAAATCACCCCTCAAGGAAACAGGATGAATTCAGTTTGGATCTG	780
QY	781	CAAAAAGGCTGCTGTGAAATTTCTGAGACGGATGTAACAATCTGACATCATCAAC	840
DB	781	CAAAAAGGCTGCTGTGAAATTTCTGAGACGGATGTAACAATCTGACATCATCAAC	840
QY	841	CCAGTAAATGATTTGAACACCACTGAGAGCGTCCAGCTGAGAGGCAATCCAGAAAAGT	900
DB	841	CCAGTAAATGATTTGAACACCACTGAGAGCGTCCAGCTGAGAGGCAATCCAGAAAAGT	900
QY	901	ATCAGGCTAGTTCTGTTTCAAACTTGCATGTGAGGCAATGTGGCAAAATATCTCATGCCA	960
DB	901	ATCAGGCTAGTTCTGTTTCAAACTTGCATGTGAGGCAATGTGGCAAAATATCTCATGCCA	960
QY	961	GCTCATTTACAGCATGAGAAACAGAGCTTTATTACTCATTAAGACAGAAATGAATGAGAA	1020
DB	961	GCTCATTTACAGCATGAGAAACAGAGCTTTATTACTCATTAAGACAGAAATGAATGAGAA	1020
QY	1021	AGGCTGAATTTCTGTAAATAAAGCAACAGAGCTTTAGCAAGAGAGCAACATCAACAGAT	1080
DB	1021	AGGCTGAATTTCTGTAAATAAAGCAACAGAGCTTTAGCAAGAGAGCAACATCAACAGAT	1080
QY	1081	GGGCTGGAAGTAAAGAAACATGTAAATGATAGGCGGACTCCAGACAGAAAAAGGTAG	1140
DB	1081	GGGCTGGAAGTAAAGAAACATGTAAATGATAGGCGGACTCCAGACAGAAAAAGGTAG	1140
QY	1141	ATCTGAATGCTGATCCCTGCTGTCAGAGAAAGAAATGCAATAAGCAGAAAACTGCATGCT	1200
DB	1141	ATCTGAATGCTGATCCCTGCTGTCAGAGAAAGAAATGCAATAAGCAGAAAACTGCATGCT	1200
QY	1201	CAGAGAACTCTTAGAGATACCTGAAGATGTTCTTCGGATAAACAATAAGCAGAAATTCAGA	1260
DB	1201	CAGAGAACTCTTAGAGATACCTGAAGATGTTCTTCGGATAAACAATAAGCAGAAATTCAGA	1260
QY	1261	AACTTAATGAGTGGTTCCTCAGAGAAATAGACTTCTGGCCAGTATCTCATGAGGCTTTAA	1320
DB	1261	AACTTAATGAGTGGTTCCTCAGAGAAATAGACTTCTGGCCAGTATCTCATGAGGCTTTAA	1320
QY	1321	GGGAGTCTGAAATCAAAATGCCAAAGTCTGATGTATTTGGACCTTCTAAATGAGGTAGTG	1380
DB	1321	GGGAGTCTGAAATCAAAATGCCAAAGTCTGATGTATTTGGACCTTCTAAATGAGGTAGTG	1380
QY	1381	AATATTTCTGCTTCTCAGAGAAATAGACTTCTGGCCAGTATCTCATGAGGCTTTAA	1440
DB	1381	AATATTTCTGCTTCTCAGAGAAATAGACTTCTGGCCAGTATCTCATGAGGCTTTAA	1440
QY	1441	TATGTAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGAGTAATTTGAAGCAAAATAT	1500
DB	1441	TATGTAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGAGTAATTTGAAGCAAAATAT	1500
QY	1501	TTGGAAAACTTATCGGAAAGAGGCTTCCCAACTTAAAGCCTTAACTGAAATTC	1560
DB	1501	TTGGAAAACTTATCGGAAAGAGGCTTCCCAACTTAAAGCCTTAACTGAAATTC	1560
QY	1561	TAAATTTAGGAGCAATTTGTTACTGAGCCACAGATAAATCAAGAGGCTCCCTCCAAATA	1620
DB	1561	TAAATTTAGGAGCAATTTGTTACTGAGCCACAGATAAATCAAGAGGCTCCCTCCAAATA	1620
QY	1621	AATTAAGCGTAAAGAGGAGCTTACATCAGGCTTCATCTCTGAGGATTTTATCAAGAAAG	1680
DB	1621	AATTAAGCGTAAAGAGGAGCTTACATCAGGCTTCATCTCTGAGGATTTTATCAAGAAAG	1680
QY	1681	CAGATTTGGCAGTTTCAAGAGCTCTGAAATGATTAATTCAGGAACTAACCCAAACGGAGC	1740
DB	1681	CAGATTTGGCAGTTTCAAGAGCTCTGAAATGATTAATTCAGGAACTAACCCAAACGGAGC	1740
QY	1741	AGAAATGGTCAAGTGAATTAATTTACTTAATAGTGGTTCATGAGAAATAAACAAGGTGAT	1800
DB	1741	AGAAATGGTCAAGTGAATTAATTTACTTAATAGTGGTTCATGAGAAATAAACAAGGTGAT	1800
QY	1801	CTATTCAGAAATGAGAAAAATCTTAAACCAATAGAAATCACTCGAAAAAGAAATCTCTTCA	1860
DB	1801	CTATTCAGAAATGAGAAAAATCTTAAACCAATAGAAATCACTCGAAAAAGAAATCTCTTCA	1860
QY	1861	AAACGAAAGCTGAACCTTAAAGCAGCAGTATTAAGCAATATGGAATTCGAATTAATATCC	1920
DB	1861	AAACGAAAGCTGAACCTTAAAGCAGCAGTATTAAGCAATATGGAATTCGAATTAATATCC	1920
QY	1921	ACAATTTCAAAAGCGCTTAAAGAAATAGGCTGAGAGGAGTCTTCTACAGGCAATATTC	1980
DB	1921	ACAATTTCAAAAGCGCTTAAAGAAATAGGCTGAGAGGAGTCTTCTACAGGCAATATTC	1980
QY	1981	ATGCGCTTGAATCTAGTGTAGTGTAGAAATCTTAAGCCCACTTAATTTGACTGAAATGCAAA	2040
DB	1981	ATGCGCTTGAATCTAGTGTAGTGTAGAAATCTTAAGCCCACTTAATTTGACTGAAATGCAAA	2040
QY	2041	TTGATAGTTGTTCTTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACCAATGCGCAGTCA	2100

Db 1921 ACAATTCAAAGCACCTTAAAGAAATAGGCTGAGGAGGAAGTCTTCTACCGGCATATTC 1980
Qy 1981 ATGCCCTTGAACTAGTACTAGTACAGTAAGATCTAAGCCCACTTAAATGTACTGAAATGCAAA 2040
Db 1981 ATGCCCTTGAACTAGTACTAGTACAGTAAGATCTAAGCCCACTTAAATGTACTGAAATGCAAA 2040
Qy 2041 TTGATAGTGTCTAGCAGTGAAGAGATGAAGAAAAAAGTAAGTAAGCAATATGCCAGTCA 2100
Db 2041 TTGATAGTGTCTAGCAGTGAAGAGATGAAGAAAAAAGTAAGTAAGCAATATGCCAGTCA 2100
Qy 2101 GGCACAGCAGAAACCTTCAACTCATGGAAGGTAAAGAACCTGCACTGAGCCCAAGAGA 2160
Db 2101 GGCACAGCAGAAACCTTCAACTCATGGAAGGTAAAGAACCTGCACTGAGCCCAAGAGA 2160
Qy 2161 GTAAACAGCCAAATGAACAGACAGTAAAGACATGACAGTGTATCTTCCAGAGCTGA 2220
Db 2161 GTAAACAGCCAAATGAACAGACAGTAAAGACATGACAGTGTATCTTCCAGAGCTGA 2220
Qy 2221 AGTTAAACAATGCACCTGGTCTTTTACTTACTAGTGTTCAAATACCAAGTCACTTAAAGAT 2280
Db 2221 AGTTAAACAATGCACCTGGTCTTTTACTTACTAGTGTTCAAATACCAAGTCACTTAAAGAT 2280
Qy 2281 TTGTCAATCTAGCCTTCCAGAGAAAGAAAGAGAGAACTAGAAAACAGTTAAAGTGT 2340
Db 2281 TTGTCAATCTAGCCTTCCAGAGAAAGAAAGAGAGAACTAGAAAACAGTTAAAGTGT 2340
Qy 2341 CTAAATATCTGAGACCCCAAGATCTCATGTAAAGTGAAGAGGGTTTGGCAACTG 2400
Db 2341 CTAAATATCTGAGACCCCAAGATCTCATGTAAAGTGAAGAGGGTTTGGCAACTG 2400
Qy 2401 AAAGATCTGTAGAGTAGCAGTATTTCACTGGTACTGGTACTGATATGGCACTCAGG 2460
Db 2401 AAAGATCTGTAGAGTAGCAGTATTTCACTGGTACTGGTACTGATATGGCACTCAGG 2460
Qy 2461 AAAGTATCTGTGAGAGTGTAGCCTCTAGGGAAGGCAAAACAGAAACCAATAAT 2520
Db 2461 AAAGTATCTGTGAGAGTGTAGCCTCTAGGGAAGGCAAAACAGAAACCAATAAT 2520
Qy 2521 GTGTGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGT 2580
Db 2521 GTGTGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGT 2580
Qy 2581 ATAAATAGAAATGACACAGAGCTTTAAAGTATCCATTTGGGAGATGAAGTAAACACATC 2640
Db 2581 ATAAATAGAAATGACACAGAGCTTTAAAGTATCCATTTGGGAGATGAAGTAAACACATC 2640
Qy 2641 GGGAAACAGCATAGAAATGGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2700
Db 2641 GGGAAACAGCATAGAAATGGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2700
Qy 2701 TCAAGGTTTCAAGGCGCCAGTCAATTTGCTCTGTTTTCAAATCCAGGAAATGCAAGAGG 2760
Db 2701 TCAAGGTTTCAAGGCGCCAGTCAATTTGCTCTGTTTTCAAATCCAGGAAATGCAAGAGG 2760
Qy 2761 AATGTGCAATCTCTGCGCACTCTGGGTCTTAAAGAAACAAAGTCAAAAGTCACTT 2820
Db 2761 AATGTGCAATCTCTGCGCACTCTGGGTCTTAAAGAAACAAAGTCAAAAGTCACTT 2820
Qy 2821 TTGAATGTGAACAAAGGAGAAATCAAGGAAGATGAGTCTAATATCAAGCTGTAC 2880
Db 2821 TTGAATGTGAACAAAGGAGAAATCAAGGAAGATGAGTCTAATATCAAGCTGTAC 2880
Qy 2881 AGACAGTTAAATATCACTGACGCTTCTGTTGGTGTGAGAAAGATAGGCAAGTGTGATA 2940
Db 2881 AGACAGTTAAATATCACTGACGCTTCTGTTGGTGTGAGAAAGATAGGCAAGTGTGATA 2940
Qy 2941 ATGCCAAATGTAGTATCAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA 3000
Db 2941 ATGCCAAATGTAGTATCAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA 3000
Qy 3001 ACGAACTGGACTCAATCTTCAAAATAAACATGAGCTTTTACAAACCCATATCGTATAC 3060
Db 3001 ACGAACTGGACTCAATCTTCAAAATAAACATGAGCTTTTACAAACCCATATCGTATAC 3060

Qy 3061 CACCACCTTTTCCCAACAGATCATTTGTTAAACCTAAATGTAAAGAAATCTGCTAGAGG 3120
Db 3061 CACCACCTTTTCCCAACAGATCATTTGTTAAACCTAAATGTAAAGAAATCTGCTAGAGG 3120
Qy 3121 AAAACCTTTGAGGACATTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAAATTCCTCA 3180
Db 3121 AAAACCTTTGAGGACATTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAAATTCCTCA 3180
Qy 3181 GTACAGTGAGCACAATTTAGCCGTAATTAACATTTAGAGAAATATGTTTTTAAAGGAGCCAGCT 3240
Db 3181 GTACAGTGAGCACAATTTAGCCGTAATTAACATTTAGAGAAATATGTTTTTAAAGGAGCCAGCT 3240
Qy 3241 CAAGCAATTTAATGAAGTAGGTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGA 3300
Db 3241 CAAGCAATTTAATGAAGTAGGTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGA 3300
Qy 3301 TAGGTTCCAGTGATGAAGAACTTCAAGCAGAACTAGGTAGAAACAGAGGGCCAAATTTGA 3360
Db 3301 TAGGTTCCAGTGATGAAGAACTTCAAGCAGAACTAGGTAGAAACAGAGGGCCAAATTTGA 3360
Qy 3361 ATGCTATGCTTAGATTTAGGGGTTTGGCACTTGAGGTCTATTAACAAAGTCTTCTG 3420
Db 3361 ATGCTATGCTTAGATTTAGGGGTTTGGCACTTGAGGTCTATTAACAAAGTCTTCTG 3420
Qy 3421 GTAAATGTAAGCATCTTGAATTAAGAAAGCAAGATATGAAGAAAGTTCAGAGTGT 3480
Db 3421 GTAAATGTAAGCATCTTGAATTAAGAAAGCAAGATATGAAGAAAGTTCAGAGTGT 3480
Qy 3481 ATACAGATTTCTTCCATATCTGATTTTCAAGTAACTTAGAAGCAAGCTTATGGGAAGTGT 3540
Db 3481 ATACAGATTTCTTCCATATCTGATTTTCAAGTAACTTAGAAGCAAGCTTATGGGAAGTGT 3540
Qy 3541 ATGCTATGCTTAGATTTAGGGGTTTGGCACTTGAGGTCTATTAACAAAGTCTTCTG 3600
Db 3541 ATGCTATGCTTAGATTTAGGGGTTTGGCACTTGAGGTCTATTAACAAAGTCTTCTG 3600
Qy 3601 AAGGATCTAGTTTGTCTGAAATGACATTAAGGAAAGTCTTCTGCTTTTGTAGCAAAAGCG 3660
Db 3601 AAGGATCTAGTTTGTCTGAAATGACATTAAGGAAAGTCTTCTGCTTTTGTAGCAAAAGCG 3660
Qy 3661 TCCAGAGGAGGAGCTTTAGCAGGAGTCTTACCCATACATTTGCTGCTCAGG 3720
Db 3661 TCCAGAGGAGGAGCTTTAGCAGGAGTCTTACCCATACATTTGCTGCTCAGG 3720
Qy 3721 GTTACCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3780
Db 3721 GTTACCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3780
Qy 3781 AAGAGCTTCCCTGCTTCCAACTTTGTTATTTGGTAAAGTAAACATATATACCTTCTCAGT 3840
Db 3781 AAGAGCTTCCCTGCTTCCAACTTTGTTATTTGGTAAAGTAAACATATATACCTTCTCAGT 3840
Qy 3841 CTACTAGGAGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3900
Db 3841 CTACTAGGAGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3900
Qy 3901 TATCATTTGAAGATAGCTTAAATGATGCTGAGTAAACAGGTAATTTGGCAAGGCACTCTC 3960
Db 3901 TATCATTTGAAGATAGCTTAAATGATGCTGAGTAAACAGGTAATTTGGCAAGGCACTCTC 3960
Qy 3961 AGGAACTACCTTTAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4020
Db 3961 AGGAACTACCTTTAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4020
Qy 4021 GTGAATTTGGAAGTCTGACTGCAATTAACAAACAGGAGGAGGAGGAGGAGGAGGAGGAGG 4080
Db 4021 GTGAATTTGGAAGTCTGACTGCAATTAACAAACAGGAGGAGGAGGAGGAGGAGGAGGAGG 4080
Qy 4081 CCAAAACAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4140
Db 4081 CCAAAACAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4140

TELEPAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; STRAIN: BRCAL
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 17
; MAP POSITION: 17q21
US-08-598-591-1

Query Match		100.0%; Score 5709.4; DB 1; Length 5711;
Best Local Similarity		100.0%; Pred. No. 0;
Matches 5710; Conservative		0; Mismatches 1; Indels 0; Gaps 0;
Qy	1	AGCTCGCTGAGACTTCTCTGGACCCCGCCAGGCTGTGGGTTCTCAGATAACTGGGCC 60
Db	1	AGCTCGCTGAGACTTCTCTGGACCCCGCCAGGCTGTGGGTTCTCAGATAACTGGGCC 60
Qy	61	CCTGGCTCAGAGGCTTCACTCTCTCTGGTAAAGTTCAATGGAAAGAAAGAA 120
Db	61	CCTGGCTCAGAGGCTTCACTCTCTCTGGTAAAGTTCAATGGAAAGAAAGAA 120
Qy	121	TGGATTATCTGCTCTCTGGGTTGAAGAGTACAAAATGTCAATTAATCTATGCAGAAAA 180
Db	121	TGGATTATCTGCTCTCTGGGTTGAAGAGTACAAAATGTCAATTAATCTATGCAGAAAA 180
Qy	181	TCTTAGAGTGTCCCATCTGCTGGAGTTGATCAGAGAACTGTCTCCCAAAAGTGTGACC 240
Db	181	TCTTAGAGTGTCCCATCTGCTGGAGTTGATCAGAGAACTGTCTCCCAAAAGTGTGACC 240
Qy	241	ACATATTTTGAATTTTGGATCTGCTGCTCAACCAAGAGAGGCTTCAACAGT 300
Db	241	ACATATTTTGAATTTTGGATCTGCTGCTCAACCAAGAGAGGCTTCAACAGT 300
Qy	301	GTCCCTTTATGTAAGATCATATAACCAAAAGAGGCTTCAAGAAAGTACGAGATTAGTC 360
Db	301	GTCCCTTTATGTAAGATCATATAACCAAAAGAGGCTTCAAGAAAGTACGAGATTAGTC 360
Qy	361	AACTTGTTCAGAGCTATTGAAATCAATTTGCTTTTCACTTGCACACAGCTTGGAGT 420
Db	361	AACTTGTTCAGAGCTATTGAAATCAATTTGCTTTTCACTTGCACACAGCTTGGAGT 420
Qy	421	ATGCAAAACAGCTATATAATTTTGCAAAAGAGGAAATAACTCTCTCTGAAACATCTAAAGATG 480
Db	421	ATGCAAAACAGCTATATAATTTTGCAAAAGAGGAAATAACTCTCTCTGAAACATCTAAAGATG 480
Qy	481	AACTTCTATCATCAAAAGTATGGCTACAGAAACCGTGCACAAAGACTTCTACAGATG 540
Db	481	AACTTCTATCATCAAAAGTATGGCTACAGAAACCGTGCACAAAGACTTCTACAGATG 540
Qy	541	AAACCCGAAATCTTCTCTGAGGAAACCAAGTCTCACTCTCACTCTCACTCTCACTCTGAA 600
Db	541	AAACCCGAAATCTTCTCTGAGGAAACCAAGTCTCACTCTCACTCTCACTCTCACTCTGAA 600
Qy	601	CTGTGAGAACTCTGAGGACAAAGCAGGAGTACAACTCTCAAAAGAGCTCTGTCTACATTG 660
Db	601	CTGTGAGAACTCTGAGGACAAAGCAGGAGTACAACTCTCAAAAGAGCTCTGTCTACATTG 660
Qy	661	AACTGGGATCTGATTTCTGAGATACCGTTTAAAGGCACTTATTCAGATGTGGAG 720
Db	661	AACTGGGATCTGATTTCTGAGATACCGTTTAAAGGCACTTATTCAGATGTGGAG 720
Qy	721	ATCAGAAATTTGTAACAATCACCCCTCAAGGACCAAGGATCAAAATCAATTTGATTTCTG 780
Db	721	ATCAGAAATTTGTAACAATCACCCCTCAAGGACCAAGGATCAAAATCAATTTGATTTCTG 780
Qy	781	CAAAAAAGGCTGCTTGTGATTTTCTGAGACGATGTAAACAAATCACTCATCAAC 840

Db	781	CAAAAAAGGCTGCTTGTGATTTTCTGAGACGATGTAAACAAATCACTCATCAAC 840
Qy	841	CCAGTAATAATGATTTTGAACACCACTGAGAGGCTGAGCTGAGAGCATCCAGAAAAGT 900
Db	841	CCAGTAATAATGATTTTGAACACCACTGAGAGGCTGAGCTGAGAGCATCCAGAAAAGT 900
Qy	901	ATCAGGCTAGTCTGTTTCAAACTTGCATGTGAGGCAATGTGGCAAAAATCTCATGCCA 960
Db	901	ATCAGGCTAGTCTGTTTCAAACTTGCATGTGAGGCAATGTGGCAAAAATCTCATGCCA 960
Qy	961	GCTCATTACAGCATGAGAACAGGAGTTTATTACTCCTCAATGAGCAGAAATGATCTAGAAA 1020
Db	961	GCTCATTACAGCATGAGAACAGGAGTTTATTACTCCTCAATGAGCAGAAATGATCTAGAAA 1020
Qy	1021	AGGCTGAATTTCTGTAATAAAGCAACAGGCTGTGGCTTTAGCAAGAGGCAACATAACAGAT 1080
Db	1021	AGGCTGAATTTCTGTAATAAAGCAACAGGCTGTGGCTTTAGCAAGAGGCAACATAACAGAT 1080
Qy	1081	GGGCTGGAAGTAAAGAAACATGTAATGATAGGAGGACTCCAGACAGAAAAAGGATG 1140
Db	1081	GGGCTGGAAGTAAAGAAACATGTAATGATAGGAGGACTCCAGACAGAAAAAGGATG 1140
Qy	1141	ATCTGAATGCTGATCCCTCTGTGAGAGAAAGATGGAATGGAATGAGCAGAACTGCCATGCT 1200
Db	1141	ATCTGAATGCTGATCCCTCTGTGAGAGAAAGATGGAATGGAATGAGCAGAACTGCCATGCT 1200
Qy	1201	CAGAGAACTCTAGAGATCTGAAAGATGTTCTTGGATTAACACTAAATAGCAGGATTCAGA 1260
Db	1201	CAGAGAACTCTAGAGATCTGAAAGATGTTCTTGGATTAACACTAAATAGCAGGATTCAGA 1260
Qy	1261	AGTTAATGAGTGGTTTCCAGAGGATGATGAACTGTTAGGCTCTGATGACTCAGATGATG 1320
Db	1261	AGTTAATGAGTGGTTTCCAGAGGATGATGAACTGTTAGGCTCTGATGACTCAGATGATG 1320
Qy	1321	GGGAGTCTGAATCAAAATGCCAAAGTACGTGATGTTTGGAGCTTCTAAATGAGGTAGTG 1380
Db	1321	GGGAGTCTGAATCAAAATGCCAAAGTACGTGATGTTTGGAGCTTCTAAATGAGGTAGTG 1380
Qy	1381	AATATTTCTGTTCTTCHAGAGAAATAGACTTCTGGCAGTGTCTCTCATGAGGCTTTAA 1440
Db	1381	AATATTTCTGTTCTTCHAGAGAAATAGACTTCTGGCAGTGTCTCTCATGAGGCTTTAA 1440
Qy	1441	TATGTAAAGTGAAGAGATTTCACTCCAAATCAGTAGAGATTAATTAATGAAGACAAATAT 1500
Db	1441	TATGTAAAGTGAAGAGATTTCACTCCAAATCAGTAGAGATTAATTAATGAAGACAAATAT 1500
Qy	1501	TTGGAAAACTTATCGGAAGAGCAAGCCTCCCAACTTAAGCCTGTAATCTGAAAATC 1560
Db	1501	TTGGAAAACTTATCGGAAGAGCAAGCCTCCCAACTTAAGCCTGTAATCTGAAAATC 1560
Qy	1561	TAATATAGAGCAATTTGTTACTGAGCCACAGATTAATCAAGAGCGTCCCTCTCAAAATA 1620
Db	1561	TAATATAGAGCAATTTGTTACTGAGCCACAGATTAATCAAGAGCGTCCCTCTCAAAATA 1620
Qy	1621	AATTAAGCGTAAAGAGACCTACATCAGGCTTCACTCTCTGAGGATTTTATCAAGAAAG 1680
Db	1621	AATTAAGCGTAAAGAGACCTACATCAGGCTTCACTCTCTGAGGATTTTATCAAGAAAG 1680
Qy	1681	CAGATTTGGCAGTTCAAAAGACTCTGAAATGATAAATCAGGGAATCAACCAAGCGAGC 1740
Db	1681	CAGATTTGGCAGTTCAAAAGACTCTGAAATGATAAATCAGGGAATCAACCAAGCGAGC 1740
Qy	1741	AGATGCTCAAGTCAATGATTAATTAATAGTGTCTCATGAGAAATTAACAAAGGATGATT 1800
Db	1741	AGATGCTCAAGTCAATGATTAATTAATAGTGTCTCATGAGAAATTAACAAAGGATGATT 1800
Qy	1801	CTATTGAGATGAGAAATCTTAACCCATAGATCACTCTGAAAGAAATCTGCTTTCA 1860
Db	1801	CTATTGAGATGAGAAATCTTAACCCATAGATCACTCTGAAAGAAATCTGCTTTCA 1860
Qy	1861	AAACGAAAGCTGAACCTTATAGCAGCAGTATAGCAATATGGAATCTGAAATTAATATCC 1920

Db 1861 AAACGAAGCTGAACCTTATAGCAGCAGTATATAGCAATATGGAATCTGAAATTAATATCC 1920
Qy 1921 ACAATTTCAAAGCAGCTAAAGAAATAGCTGAGGAGGAAGTCTTCTACCAAGGATATTC 1980
Db 1921 ACAATTTCAAAGCAGCTAAAGAAATAGCTGAGGAGGAAGTCTTCTACCAAGGATATTC 1980
Qy 1981 ATGCGCTTGAAGTGTAGTCTAGTAGAATCTTAAGCCCACTTAATTTGTAATGTAATGCAAA 2040
Db 1981 ATGCGCTTGAAGTGTAGTCTAGTAGAATCTTAAGCCCACTTAATTTGTAATGTAATGCAAA 2040
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACCAAAATGCCAGTCA 2100
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACCAAAATGCCAGTCA 2100
Qy 2101 GGCAAGCAGAAACCTTACAACTCATGAGGAAGTAAAGAACCTTGCACTCGGAGCCCAAGAGA 2160
Db 2101 GGCAAGCAGAAACCTTACAACTCATGAGGAAGTAAAGAACCTTGCACTCGGAGCCCAAGAGA 2160
Qy 2161 GTAACAGCCAAATGAACAGACCAAGTAAAGACATGACAGTGATCTTCCACAGAGTGA 2220
Db 2161 GTAACAGCCAAATGAACAGACCAAGTAAAGACATGACAGTGATCTTCCACAGAGTGA 2220
Qy 2221 AGTTAAACAAATGCACTCGGTTCTTTTACTAAGTGTCAAATACCAGTGAATCTTAAGAAAT 2280
Db 2221 AGTTAAACAAATGCACTCGGTTCTTTTACTAAGTGTCAAATACCAGTGAATCTTAAGAAAT 2280
Qy 2281 TTGTCAATCTTAGCCTTCCAGAGAGAAAGAAAGAGAGCACTAGAAACAGTCTTAAGTGT 2340
Db 2281 TTGTCAATCTTAGCCTTCCAGAGAGAAAGAAAGAGAGCACTAGAAACAGTCTTAAGTGT 2340
Qy 2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAAGTGGAGAAAGGGTTTGCAAACTG 2400
Db 2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAAGTGGAGAAAGGGTTTGCAAACTG 2400
Qy 2401 AAGATCTGTAGAGAGTAGAGTATTTTCACTGGTACCTGGTACTGATTTATGGCTCAGG 2460
Db 2401 AAGATCTGTAGAGAGTAGAGTATTTTCACTGGTACCTGGTACTGATTTATGGCTCAGG 2460
Qy 2461 AAGATCTCTGTTACTGGAAGTTAGCACTCTAGGAGAGGCCAAACACAGAAACCAATTAAT 2520
Db 2461 AAGATCTCTGTTACTGGAAGTTAGCACTCTAGGAGAGGCCAAACACAGAAACCAATTAAT 2520
Qy 2521 GTGTGAGTCAGTGTGACGATTTGAAACCCCAAGGAGCAATATTCATGTTGTTTCCAAAG 2580
Db 2521 GTGTGAGTCAGTGTGACGATTTGAAACCCCAAGGAGCAATATTCATGTTGTTTCCAAAG 2580
Qy 2581 ATAATAGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAACACAGTC 2640
Db 2581 ATAATAGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAACACAGTC 2640
Qy 2641 GGGAAACCAAGCATAGAAATGGAAGAAAGTGAATCTGATGCTCAGTATTTGCGAATAAT 2700
Db 2641 GGGAAACCAAGCATAGAAATGGAAGAAAGTGAATCTGATGCTCAGTATTTGCGAATAAT 2700
Qy 2701 TCAAGGTTTCAAGGCGCAGTCATTTGCTCTGTTTCAATCCAGGAAATCCAGAGAGG 2760
Db 2701 TCAAGGTTTCAAGGCGCAGTCATTTGCTCTGTTTCAATCCAGGAAATCCAGAGAGG 2760
Qy 2761 AATGTCAACATTTCTCTGCCACTCTGGGTCCTTTAAGAAACCAAGTCCAAAGTCACTT 2820
Db 2761 AATGTCAACATTTCTCTGCCACTCTGGGTCCTTTAAGAAACCAAGTCCAAAGTCACTT 2820
Qy 2821 TTGAATGTGAACAAAGAAAGAAATCAAGGAAAGATGAGTCTTAATATCAAGCTGTAC 2880
Db 2821 TTGAATGTGAACAAAGAAAGAAATCAAGGAAAGATGAGTCTTAATATCAAGCTGTAC 2880
Qy 2881 AGACAGTTTAATATCACTCAGGCTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2940
Db 2881 AGACAGTTTAATATCACTCAGGCTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2940
Qy 2941 ATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGCA 3000
Db 2941 ATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGCA 3000

Qy 3001 ACGAACCTGACCTCATTTACTCCAAATAAACAATGCACTTTTACAAAACCCATATCGTATAC 3060
Db 3001 ACGAACCTGACCTCATTTACTCCAAATAAACAATGCACTTTTACAAAACCCATATCGTATAC 3060
Qy 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAAATGTAAGAAATCTCTGTAGAGG 3120
Db 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAAATGTAAGAAATCTCTGTAGAGG 3120
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Qy 3181 GTACAGTGAGCAAAATTTAGCCGTAATAACAATTAGAGAAATGTTTTTAAAGAGGCCAGCT 3240
Db 3181 GTACAGTGAGCAAAATTTAGCCGTAATAACAATTAGAGAAATGTTTTTAAAGAGGCCAGCT 3240
Qy 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAGA 3300
Db 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAGA 3300
Qy 3301 TAGGTTCCAGTGATGAAACATTTCAAGCAGAACTAGGTAGAAACAGAGGGCCAAAATTTGA 3360
Db 3301 TAGGTTCCAGTGATGAAACATTTCAAGCAGAACTAGGTAGAAACAGAGGGCCAAAATTTGA 3360
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Db 3361 ATGCTATGCTTACATTTAGGAGGTTTTCGCACTGAGGCTCTATTAACAAAGTCTTCTCGGAA 3420
Qy 3421 GTAAATGTAAGCATCTGAAATAAAAAGCAAGAAATGAAGAGTAGTTTCAGACTGTTA 3480
Db 3421 GTAAATGTAAGCATCTGAAATAAAAAGCAAGAAATGAAGAGTAGTTTCAGACTGTTA 3480
Qy 3481 ATACAGATTTCTCTCCATATCTCATTTAGGAGGTTTTCGCACTGAGGCTCTATTAACAAAGTCT 3540
Db 3481 ATACAGATTTCTCTCCATATCTCATTTAGGAGGTTTTCGCACTGAGGCTCTATTAACAAAGTCT 3540
Qy 3541 ATGCTATCTCAGGTTTGTCTGACAGCCTGATGACCTGTTAGATGATGATGATGATGATGATG 3600
Db 3541 ATGCTATCTCAGGTTTGTCTGACAGCCTGATGACCTGTTAGATGATGATGATGATGATGATG 3600
Qy 3601 AAGATCTAGTTTGTCTGAAATGCAATTAAGGAAAGTCTGCTGTTTGTAGCAAAAGCG 3660
Db 3601 AAGATCTAGTTTGTCTGAAATGCAATTAAGGAAAGTCTGCTGTTTGTAGCAAAAGCG 3660
Qy 3661 TCCAGAGAGGAGAGCTTAGCAGAGTCTTAGCCCTTTTCCACCATACACATTTGCGCTCAGG 3720
Db 3661 TCCAGAGAGGAGAGCTTAGCAGAGTCTTAGCCCTTTTCCACCATACACATTTGCGCTCAGG 3720
Qy 3721 GTTACCGAGAGGGGCCAAGAAATTAAGTCTCTCAGAGAACTTATCTAGTGTAGGATG 3780
Db 3721 GTTACCGAGAGGGGCCAAGAAATTAAGTCTCTCAGAGAACTTATCTAGTGTAGGATG 3780
Qy 3781 AAGAGCTTCTCTCTTCCAACTGTTTATTTGGTAAAGTAAACAATATACCTTTCTCAGT 3840
Db 3781 AAGAGCTTCTCTCTTCCAACTGTTTATTTGGTAAAGTAAACAATATACCTTTCTCAGT 3840
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Db 3841 CTACTAGGCATAGCAACGTTGCTTACCGAGTCTGTCTAAGAACACAGAGGAGAAATTTAT 3900
Qy 3901 TATCATTTGAGAGTACTTAATGATCTGAGTAAACAGGTAACAGGTAATTTGGCAAGGCACTTC 3960
Db 3901 TATCATTTGAGAGTACTTAATGATCTGAGTAAACAGGTAACAGGTAATTTGGCAAGGCACTTC 3960
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Db 3961 AGGAACATCACTTACTGAGGAAACAAAATGTTTCTGCTAGCTTGTGTTTCTTCAAGTGCA 4020
Qy 4021 GTGAATTTGAGAGCTTGACTGCNAATACAAACCCAGGATCTTCTTCTTGTGATGTTGTTCTT 4080
Db 4021 GTGAATTTGAGAGCTTGACTGCNAATACAAACCCAGGATCTTCTTCTTGTGATGTTGTTCTT 4080

4081 CCAACAAATGAGGATCAGTCTGAAAGCCAGGAGTTGGTCTCAGTGCACAGGAAATGG 4140
Db CCAACAAATGAGGATCAGTCTGAAAGCCAGGAGTTGGTCTCAGTGCACAGGAAATGG 4140
4141 TTTGAGATGATGAG 4200
Db TTTGAGATGATGAG 4200
4201 TGGATTCAAACTTAGTGAAGCAGCATCTGGGTGTGAGAGTGAACAGAGCCTCTCTGAAG 4260
Db TGGATTCAAACTTAGTGAAGCAGCATCTGGGTGTGAGAGTGAACAGAGCCTCTCTGAAG 4260
4261 ACTGCTCAGAGGTATCTCTCAGAGTGACATTTTAACCACTCAGCAGAGGAGATCAGTGC 4320
Db ACTGCTCAGAGGTATCTCTCAGAGTGACATTTTAACCACTCAGCAGAGGAGATCAGTGC 4320
4321 AACATAAATCTGATAAAGCTCCAGCAGGAGAAATGGCTGAACACTAGAGCTGTGTAGAACAGC 4380
Db AACATAAATCTGATAAAGCTCCAGCAGGAGAAATGGCTGAACACTAGAGCTGTGTAGAACAGC 4380
4381 ATGGAGCCAGCCTTCTAACAGTACCTTCCATCATTAAGTGACTCTTCTGCCCTTGAGG 4440
Db ATGGAGCCAGCCTTCTAACAGTACCTTCCATCATTAAGTGACTCTTCTGCCCTTGAGG 4440
4441 ACCTGCGAAATCCAGAACCAAGCAGATCAGAAAGAGAGAGTAACTTCAAGAAAGTAA 4500
Db ACCTGCGAAATCCAGAACCAAGCAGATCAGAAAGAGAGAGTAACTTCAAGAAAGTAA 4500
4501 GTGAATACCTATTAAGCCAGAGATCCAGAGAGCCTTTCTGCTGACAGAGTTGAGGTGCTG 4560
Db GTGAATACCTATTAAGCCAGAGATCCAGAGAGCCTTTCTGCTGACAGAGTTGAGGTGCTG 4560
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Db CAGATAGTCTACAGTAAATTAAGAACAGAGAGTGAAGTCACTCCCTCTTAAT 4620
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Db GCCCATCATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4680
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Db ACTACCCATCTCAAGAGAGTCAATTAAGTTGTTGATGTTGAGAGAGAGAGAGAGAGAG 4740
4741 AGTCTGCGCCACAGATTTGCGGAAACATCTTACTTCCAGGAGAGAGATCTAGAGGAA 4800
Db AGTCTGCGCCACAGATTTGCGGAAACATCTTACTTCCAGGAGAGAGATCTAGAGGAA 4800
4801 CCCCTTACCTGGAATCTGGAATCAGCCTCTTCTCTGATGACCCCTGAATCTGATCCTCTG 4860
Db CCCCTTACCTGGAATCTGGAATCAGCCTCTTCTCTGATGACCCCTGAATCTGATCCTCTG 4860
4861 AAGCAG 4920
Db AAGCAG 4920
4921 AAGTTTCCCAATTAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4980
Db AAGTTTCCCAATTAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4980
4981 ATACTGCTGGGTATTAATCCATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 5040
Db ATACTGCTGGGTATTAATCCATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 5040
5041 CTTCAACAG 5100
Db CTTCAACAG 5100
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Db AATTTATGCTGTGATCAAGTTTGCAGAAACCAACATCACTTAATTAATTAATTAATTA 5160
5161 CTGAAGAGAGACTACTCATCTGTTATGAAACAGAGTGTGAGTTTGTGTGAGAGAGAG 5220

5161 CTGAAGAGAGACTACTCATCTGTTTATGAAACAGATGCTGAGTTGTGTGTGAGAGAGAG 5220
Qy TGAATAATTTCTAGAGATTTGCGGAGAGAAATGGGTAGTTAGTATTTCTGGGTGACCC 5280
Db TGAATAATTTCTAGAGATTTGCGGAGAGAAATGGGTAGTTAGTATTTCTGGGTGACCC 5280
5281 AGTCTATTAAAGAAAGAAAAATCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG 5340
Db AGTCTATTAAAGAAAGAAAAATCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG 5340
5341 TCATGCAAGAAACCCACCAAGGTCCTAAGCGGACAGAGAAATCCACAGGACAGAAAGATCT 5400
Db TCATGGAAGAAACCCACCAAGGTCCTAAGCGGACAGAGAAATCCACAGGACAGAAAGATCT 5400
5401 TCAGGGGGCTAGAAATCTGTTGCTATGGGGCCCTTCAACCAATGATGATCACTCACTGG 5460
Db TCAGGGGGCTAGAAATCTGTTGCTATGGGGCCCTTCAACCAATGATGATCACTCACTGG 5460
5461 AATGATGTTACAGCTGTGTGCTTCTGTTGAGGAGCTTTCATCATTTCACTTCACTGG 5520
Db AATGATGTTACAGCTGTGTGCTTCTGTTGAGGAGCTTTCATCATTTCACTTCACTGG 5520
5521 GCACAGGTGTCACCCCAATTTGTTGTGTCAGGAGAGATGCTGCAAGAGGACAAATGGCT 5580
Db GCACAGGTGTCACCCCAATTTGTTGTGTCAGGAGAGATGCTGCAAGAGGACAAATGGCT 5580
5581 TCCATGCAATTTGGGAGATGTGAGGACCTTGTGAGGAGAGAGAGAGAGAGAGAGAGAG 5640
Db TCCATGCAATTTGGGAGATGTGAGGACCTTGTGAGGAGAGAGAGAGAGAGAGAGAGAG 5640
5641 GTGTAGCACTTACCACTGTCAGGAGCTGAGACCTTACCTGATACCCAGATCCCCCA 5700
Db GTGTAGCACTTACCACTGTCAGGAGCTGAGACCTTACCTGATACCCAGATCCCCCA 5700
5701 GCCACTACTGA 5711
Db GCCACTACTGA 5711

RESULT 5

US-08-798-691-1
; Sequence 1, Application US/08798691
; Patent No. 5750400
; GENERAL INFORMATION:
; APPLICANT: Murphy, Patricia D.
; APPLICANT: Allen, Antoinette C.
; APPLICANT: Alvares, Christopher P.
; APPLICANT: Critz, Brenda S.
; APPLICANT: Olson, Sheri J.
; APPLICANT: Schelter, Denise B.
; APPLICANT: Zeng, Bin
; TITLE OF INVENTION: Coding Sequences of the Human
; TITLE OF INVENTION: BRCA1 Gene
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ONCORMED
; STREET: 200 Perry Parkway
; CITY: Gaithersburg
; STATE: MD
; COUNTRY: USA
; ZIP: 20877
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,691
; FILING DATE: 12-Feb-97
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas Gallegos

REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: PA-0054CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-527-2051
TELEFAX: 301-208-6997
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCAL
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
US-08-798-691-1

Query Match 100.0%; Score 5709.4; DB 1; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	AGCTCGCTGAGACTTCCTGAGACCCGACACAGGCTGTGGGTTTCTCAGATPAACTGGGCC	60
Db	1	AGCTCGCTGAGACTTCCTGAGACCCGACACAGGCTGTGGGTTTCTCAGATPAACTGGGCC	60
Qy	61	CCTGGCTCAGAGGCTTCACCTCTGCTGCTGGGTAAAGTTCAATGGAAACAGAAAGAA	120
Db	61	CCTGGCTCAGAGGCTTCACCTCTGCTGCTGGGTAAAGTTCAATGGAAACAGAAAGAA	120
Qy	121	TGGATTATCTGCTCTTCGCGTTGAGAAAGTACAAAATGTCATTAATGCTATGAGAA	180
Db	121	TGGATTATCTGCTCTTCGCGTTGAGAAAGTACAAAATGTCATTAATGCTATGAGAA	180
Qy	181	TCCTAGAGTGCCTATCTGCTGAGTTGATCAAGGACCTGCTCCACAAAGTGTGACC	240
Db	181	TCCTAGAGTGCCTATCTGCTGAGTTGATCAAGGACCTGCTCCACAAAGTGTGACC	240
Qy	241	ACATATTTTGCAAAATTTTGCAATGCTGAACTTCTCAACGAGAAAGAGGCTTTCACAGT	300
Db	241	ACATATTTTGCAAAATTTTGCAATGCTGAACTTCTCAACGAGAAAGAGGCTTTCACAGT	300
Qy	301	GTCCTTTATGTAAGATATATACCAAGAGGACCTACAGAAAGTACAGATTTAGTC	360
Db	301	GTCCTTTATGTAAGATATATACCAAGAGGACCTACAGAAAGTACAGATTTAGTC	360
Qy	361	AACCTTTGTAAGAGCTATTGAAATCATTTTGCTTTTTCAGTTTGACACAGGTTTGAGT	420
Db	361	AACCTTTGTAAGAGCTATTGAAATCATTTTGCTTTTTCAGTTTGACACAGGTTTGAGT	420
Qy	421	ATGCAACAGCTATAATTTTGCAAAAGAGAAATTAATCTCTCGAACATCTAAAGATG	480
Db	421	ATGCAACAGCTATAATTTTGCAAAAGAGAAATTAATCTCTCGAACATCTAAAGATG	480
Qy	481	AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG	540
Db	481	AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG	540
Qy	541	AACCGGAAATCTCTTCTTGAGGAAACCACTCTCAGTGTCCAACTCTCTAACTTGAA	600
Db	541	AACCGGAAATCTCTTCTTGAGGAAACCACTCTCAGTGTCCAACTCTCTAACTTGAA	600
Qy	601	CTGTGAGAACTCTGAGGACCAAGCGGATACAACTCTCAAGACGCTGCTCTACATTG	660
Db	601	CTGTGAGAACTCTGAGGACCAAGCGGATACAACTCTCAAGACGCTGCTCTACATTG	660
Qy	661	AATGGGATCTGATCTTCTGAGATACCGTTAATAGGCACTTATTCAGTGTGGAG	720
Db	661	AATGGGATCTGATCTTCTGAGATACCGTTAATAGGCACTTATTCAGTGTGGAG	720
Qy	721	ATCAAGATTGTTACAAATCACCCCTCAAGGACCGGATGAATCAGTTTGATTCTG	780

Db	721	ATCAAGATTGTTACAAATCACCCCTCAAGGACCGGATGAATCAGTTTGATTCTG	780
Qy	781	CAAAAAGGCTGCTTGTGTAATTTCTGAGACGGATGTAACAATATCTGAACATCATCAAC	840
Db	781	CAAAAAGGCTGCTTGTGTAATTTCTGAGACGGATGTAACAATATCTGAACATCATCAAC	840
Qy	841	CCAGTAATATGATTTTGAACACCACTGAGAGCGTGCAGCTGAGAGGCTATCCAGAAAGT	900
Db	841	CCAGTAATATGATTTTGAACACCACTGAGAGCGTGCAGCTGAGAGGCTATCCAGAAAGT	900
Qy	901	ATCAGGTTAGTTCTGTTTCAAACTTGATGTGGAGCCATGTGGCAAAATATCTATGCGCA	960
Db	901	ATCAGGTTAGTTCTGTTTCAAACTTGATGTGGAGCCATGTGGCAAAATATCTATGCGCA	960
Qy	961	GCTCATTACAGCATGAGAACAGCAGTTTATTCTACTATAAGACACAAATGAATGTAGAAA	1020
Db	961	GCTCATTACAGCATGAGAACAGCAGTTTATTCTACTATAAGACACAAATGAATGTAGAAA	1020
Qy	1021	AGGCTGAAATTTCTGTAAATAAAGCAACAGCTGGCTTAGCAAGGCCCAACATACAGAT	1080
Db	1021	AGGCTGAAATTTCTGTAAATAAAGCAACAGCTGGCTTAGCAAGGCCCAACATACAGAT	1080
Qy	1081	GGGCTCGAAGTAAAGAACATGTATGATAGCGGACTCCAGACAGAAAGAAAGGTAG	1140
Db	1081	GGGCTCGAAGTAAAGAACATGTATGATAGCGGACTCCAGACAGAAAGAAAGGTAG	1140
Qy	1141	ATCTGAATGCTGATCCCTCTGTGTGAGAGAAAGAAATGGAATAGCAGAAATGCCCATGCT	1200
Db	1141	ATCTGAATGCTGATCCCTCTGTGTGAGAGAAAGAAATGGAATAGCAGAAATGCCCATGCT	1200
Qy	1201	CAGAGATCTAGAGATCTGAAGATGTTCTTGGATACACTAATAGCAGCATTCAGA	1260
Db	1201	CAGAGATCTAGAGATCTGAAGATGTTCTTGGATACACTAATAGCAGCATTCAGA	1260
Qy	1261	AACTTAATGAGTGGTTTCCAGAAAGTATGAACCTGTTAGGTTCTGATGACTCACATGATG	1320
Db	1261	AACTTAATGAGTGGTTTCCAGAAAGTATGAACCTGTTAGGTTCTGATGACTCACATGATG	1320
Qy	1321	GGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTATTGAGCGTTCTAAATAGGTTAGATG	1380
Db	1321	GGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTATTGAGCGTTCTAAATAGGTTAGATG	1380
Qy	1381	AATATTCTGTTCTTCAGAGAAATATAGCTTACTGCGCAGTGTATCTCATGAGGCTTTAA	1440
Db	1381	AATATTCTGTTCTTCAGAGAAATATAGCTTACTGCGCAGTGTATCTCATGAGGCTTTAA	1440
Qy	1441	TATGTAAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATAATTTGAAGACAAATAT	1500
Db	1441	TATGTAAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATAATTTGAAGACAAATAT	1500
Qy	1501	TTGGGAAACCTTATCGAAGAGGCGAGCTCCCAACTTAACTTAACTGTAATCTGAAATC	1560
Db	1501	TTGGGAAACCTTATCGAAGAGGCGAGCTCCCAACTTAACTTAACTGTAATCTGAAATC	1560
Qy	1561	TAAATATAGAGCATTTGTTTACTGAGCCACAGATAATACAGAGCGTCCCTCCACAAATA	1620
Db	1561	TAAATATAGAGCATTTGTTTACTGAGCCACAGATAATACAGAGCGTCCCTCCACAAATA	1620
Qy	1621	AATTAAGCGTAAAGGAGACCTACATCAGGCTTCACTCTGAGGATTTTATCAAGAAAG	1680
Db	1621	AATTAAGCGTAAAGGAGACCTACATCAGGCTTCACTCTGAGGATTTTATCAAGAAAG	1680
Qy	1681	CAGATTGGCAGTTCAAAAGACTCTCTGAAATGATAATCAGGGAACTAAACAAACGAGC	1740
Db	1681	CAGATTGGCAGTTCAAAAGACTCTCTGAAATGATAATCAGGGAACTAAACAAACGAGC	1740
Qy	1741	AGAAATGCTCAAGTGAATATTTACTTAATAGTGGTCTATGAGATATAAACAAGGTTGATT	1800
Db	1741	AGAAATGCTCAAGTGAATATTTACTTAATAGTGGTCTATGAGATATAAACAAGGTTGATT	1800
Qy	1801	CTAATTCAGATGAGAAATATCCCTTAACCCCAATAGAACTCACTCGAAAGAAATCTGCTTCA	1860

Db 1801 CTATTGAGAAATGAGAAATCTTAACCCAAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA 1860
QY 1861 AAAAGAAAGCTGAACCTTATAGCAGCAGTATAAGCAATATGGAACCTCGAATTAATATCC 1920
Db 1861 AAACGAAAGCTGAACCTTATAGCAGCAGTATAAGCAATATGGAACCTCGAATTAATATCC 1920
QY 1921 ACAATTCAAAGACCTTAAAGAAATAGGCTGAGGAGAGTCTTCTACAGGCAATATTC 1980
Db 1921 ACAATTCAAAGACCTTAAAGAAATAGGCTGAGGAGAGTCTTCTACAGGCAATATTC 1980
QY 1981 ATGGCTTGTAAGTACTAGTACTAGTAAATCTTAAGCCCACTTAATTTGACTGAAATTCGAAA 2040
Db 1981 ATGGCTTGTAAGTACTAGTACTAGTAAATCTTAAGCCCACTTAATTTGACTGAAATTCGAAA 2040
QY 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAACCAATGCGAGTCA 2100
Db 2101 GGCAAGCAGAAAACTTCAACTCATGAGAGTAAAGAACCTGCAACTGGAGCCCAAGAGA 2160
Db 2101 GGCAAGCAGAAAACTTCAACTCATGAGAGTAAAGAACCTGCAACTGGAGCCCAAGAGA 2160
QY 2161 GTAAACAGCCAAATGAAACAGACAAATGAAAGACATGACAGTGAATCTTCCAGAGCTGA 2220
Db 2161 GTAAACAGCCAAATGAAACAGACAAATGAAAGACATGACAGTGAATCTTCCAGAGCTGA 2220
QY 2221 AGTTAAACAAATGCACCTGGTCTTTTACTAAGTGTTCMAATPACAGTGAACCTTAAGAAAT 2280
Db 2221 AGTTAAACAAATGCACCTGGTCTTTTACTAAGTGTTCMAATPACAGTGAACCTTAAGAAAT 2280
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QY 2341 CTAATAATCTGGAAGACCCCAAGATCTCATGTTAAAGTGGAGAAAGGGTTTTGCAAACTG 2400
Db 2341 CTAATAATCTGGAAGACCCCAAGATCTCATGTTAAAGTGGAGAAAGGGTTTTGCAAACTG 2400
QY 2401 AAGATCTGTAGAGAGTACAGTATTTCACTGTGTACTGTGTACTGATTTATGCGCACTCAGG 2460
Db 2401 AAGATCTGTAGAGAGTACAGTATTTCACTGTGTACTGTGTACTGATTTATGCGCACTCAGG 2460
QY 2461 AAAGTATCTGCTGTAAGAGTGTAGCACTCTAGGGAAGGCAAAACAGAAACCAATTAAT 2520
Db 2461 AAAGTATCTGCTGTAAGAGTGTAGCACTCTAGGGAAGGCAAAACAGAAACCAATTAAT 2520
QY 2521 GTGTGAGTGTGCGAGATTTGAAACCCCAAGGAGTAAATCACTGTTGTTCCAAAG 2580
Db 2521 GTGTGAGTGTGCGAGATTTGAAACCCCAAGGAGTAAATCACTGTTGTTCCAAAG 2580
QY 2581 ATAATAGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAAACCACTG 2640
Db 2581 ATAATAGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAAACCACTG 2640
QY 2641 GGGAAACAGCATAGAAATGGAGAAAGTGAATCTGATGCTCAGTATTTGAGAAATACAT 2700
Db 2641 GGGAAACAGCATAGAAATGGAGAAAGTGAATCTGATGCTCAGTATTTGAGAAATACAT 2700
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Db 2701 TCAAGGTTTTCAAGCGCCAGTCAATTTGCTGTTTTCAATCCAGGAAATGCGAGAGG 2760
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Db 2761 AATGCGCAATTTCTCTGCCACTCTGGGCTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820
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Db 2821 TTGAAATGTAACAAAGAGAGAAATCAAGGAAAGTCAAGTCAATTAATCAAGCTGTAC 2880
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Db 2881 AGACAGTTTAATATCACTGAGGCTTTCTGCTGTTGGTTCAGAAAGATAAGCCAGTTGATA 2940

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Qy	4141	TTTCAGATGATGAAGAAAGAGGAACCGGCTTTGGAGAAGAAATATATCAAGAAAGACGAAGCA	4200
Db	4141	TTTCAGATGATGAAGAAAGAGGAACCGGCTTTGGAGAAGAAATATATCAAGAAAGACGAAGCA	4200
Qy	4201	TGGATTCAAACTTAGGTGACGACGATCTCGGTGTGAGAGTGAAGAAACAAGCGTCTCTGGAAG	4260
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Qy	4261	ACTGCTCAGGGCTATCCTCTCTCAGAGTGACATATTTAAACCACTCAGCAGAGAGGATACCATGC	4320
Db	4261	ACTGCTCAGGGCTATCCTCTCTCAGAGTGACATATTTAAACCACTCAGCAGAGAGGATACCATGC	4320
Qy	4321	AACATAACCTGNTAAGCTCCAGCAGGAATGGCTGAACTTAGAAGCTGTGTTAGACAGC	4380
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Qy	4561	CAGATAGTTCTTACAGTAAAAATAAGAAACAGAGGTGGAAGGTGATCCCTTCTAAAT	4620
Db	4561	CAGATAGTTCTTACAGTAAAAATAAGAAACAGAGGTGGAAGGTGATCCCTTCTAAAT	4620
Qy	4621	GCCCATCATTAGATGATAGTGTGTACATGCACAGTTGTCTCTGCGGAGTCTTCAAGATAGAA	4680
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Db	4861	AAGACAGAGCCCCAGATGTCAGTCTGTTGGCAACATACCATCTTCAAACCTCTGCAATTGA	4920
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Db	4981	ATATCTGCTGGGTATAATATGGAAGAAAGTGTGACAGGGAGAAAGCCAGAAATTGACAG	5040
Qy	5041	CTTTCACAGGAAGGCTCAACAAAGATATTCATGTTGGTGTCTGCGCTCGACCCCAAG	5100
Db	5041	CTTTCACAGGAAGGCTCAACAAAGATATTCATGTTGGTGTCTGCGCTCGACCCCAAG	5100
Qy	5101	AAATTTATGCTCGTGTACAAAGTTTTCAGAGAAAACACCAATCATCTTTTAATCTAATTA	5160

5101	Db		AAITATGCTCGGTGACAGTTTGCCAGAAAACACACATCACTTAACTAATCTAATTA	5160
5161	Qy		CTGAGAGACTACTCAATGTTGTTATGAAAACAGATGCTGAGTTTGTTGTGTAACGGACAC	5220
5161	Db		CTGAGAGACTACTCAATGTTGTTATGAAAACAGATGCTGAGTTTGTTGTGTAACGGACAC	5220
5221	Qy		TGAATATTTTCTAGGAAATTGCGGGAGGAAAAATGGGTAGTTAGCTATTTCTGGGTGACCC	5280
5221	Db		TGAATATTTTCTAGGAAATTGCGGGAGGAAAAATGGGTAGTTAGCTATTTCTGGGTGACCC	5280
5281	Qy		AGTCTATTAAAGAAAGAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG	5340
5281	Db		AGTCTATTAAAGAAAGAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG	5340
5341	Qy		TCAATGGAAGAACCAACCAAGGTCCTCAAGGGCAAGAGATCCCAAGGACAGAGAAATCT	5400
5341	Db		TCAATGGAAGAACCAACCAAGGTCCTCAAGGGCAAGAGATCCCAAGGACAGAGAAATCT	5400
5401	Qy		TCAGGGGGCTAGAAAATCTGTTGCTATGGGCCCTTTCACCAACATGCCACAGATCAACTGG	5460
5401	Db		TCAGGGGGCTAGAAAATCTGTTGCTATGGGCCCTTTCACCAACATGCCACAGATCAACTGG	5460
5461	Qy		AATGGAATGTPACAGCTGTGTGTGCTCTGTGTGTGAAGAGCTTTTCATCATTCACCCCTTG	5520
5461	Db		AATGGAATGTPACAGCTGTGTGTGCTCTGTGTGTGAAGAGCTTTTCATCATTCACCCCTTG	5520
5521	Qy		GCACAGGTGCCACCCAAATTGTGGTTGTGCAGCCAGATGCTCGACAGAGGACAAATGGCT	5580
5521	Db		GCACAGGTGCCACCCAAATTGTGGTTGTGCAGCCAGATGCTCGACAGAGGACAAATGGCT	5580
5581	Qy		TCCATGCAATTTGGGCGAGATGTTGAGGACCTGTGTGTGACCCGAGAGTGGGTGTTGGACA	5640
5581	Db		TCCATGCAATTTGGGCGAGATGTTGAGGACCTGTGTGTGACCCGAGAGTGGGTGTTGGACA	5640
5641	Qy		GTGTAGCACTCTACCAAGTGCCAGGAGCTGACACCTTACCTGATACCCAGATCCCCCACA	5700
5641	Db		GTGTAGCACTCTACCAAGTGCCAGGAGCTGACACCTTACCTGATACCCAGATCCCCCACA	5700
5701	Qy		GCCACTACTGA 5711	
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RESULT 6
US-08-825-487A-1
Sequence 1, Application US/08825487A
Patent No. 6048689
GENERAL INFORMATION:
APPLICANT: MURPHY, Patricia D.
APPLICANT: WHITE, MARGA B.
TITLE OF INVENTION: METHODS FOR IDENTIFYING VARIATIONS IN POLYNUCLEOTIDE SEQUENC
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue., N.W.
CITY: Washington,
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/825,487A
FILING DATE: 28-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/060002
FILING DATE: 26-MAR-1998
CLASSIFICATION: 435

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8100
TELEFAX: 650-463-8400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCAL
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
US-08-825-487A-1

Query Match 100.0%; Score 5709, 4; DB 3; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 5101 AATTTATGCTGCTGTACAGTTTCCAGAAAACACACATCATCTTTAACTAACTAATTA 5160
Qy 5161 CTGAAGAGACTACTCATCTGTTTATGAAAACAGATGCTGAGTTTGTGTGAAACGGACAC 5220
Db 5161 CTGAAGAGACTACTCATCTGTTTATGAAAACAGATGCTGAGTTTGTGTGAAACGGACAC 5220
Qy 5221 TGAATAATTTCTAGGAATTCGGAGGAAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280
Db 5221 TGAATAATTTCTAGGAATTCGGAGGAAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280
Qy 5281 AGTCTATTAAAGAAAAGAAAATGCTGAATGAGCATGATTTTGAAGTCAAGGAGATGTGG 5340
Db 5281 AGTCTATTAAAGAAAAGAAAATGCTGAATGAGCATGATTTTGAAGTCAAGGAGATGTGG 5340
Qy 5341 TCAATGGAAGAAACCAACAAGGTTCCAAAGCGAGCAGAGATCCAGGACAGAAAGATCT 5400
Db 5341 TCAATGGAAGAAACCAACAAGGTTCCAAAGCGAGCAGAGATCCAGGACAGAAAGATCT 5400
Qy 5401 TCAGGGGCTAGAAAATCTGTTGCTATGCGGCCCTTCCAAACATCCCAAGATCAACTGG 5460
Db 5401 TCAGGGGCTAGAAAATCTGTTGCTATGCGGCCCTTCCAAACATCCCAAGATCAACTGG 5460
Qy 5461 AATGATGCTGACAGCTGTGTGCTTCTGTGTGTAAGAGGAGCTTTCATCTACCCCTTG 5520
Db 5461 AATGATGCTGACAGCTGTGTGCTTCTGTGTGTAAGAGGAGCTTTCATCTACCCCTTG 5520
Qy 5521 GCACAGTGTCCACCCAAATTTGTGTTGCTGAGCAGATGCTGCAAGAGGAGCAATGGCT 5580
Db 5521 GCACAGTGTCCACCCAAATTTGTGTTGCTGAGCAGATGCTGCAAGAGGAGCAATGGCT 5580
Qy 5581 TCCATGCAATTTGGCAGATGTGTGAGGACCTGTGTGAGCCGAGAGTGGGTGTTGGACA 5640
Db 5581 TCCATGCAATTTGGCAGATGTGTGAGGACCTGTGTGAGCCGAGAGTGGGTGTTGGACA 5640
Qy 5641 GTGTAGCACTCTACAGTCCAGGAGCTGAGCAGCTGATGATACCCAGATCCCCACA 5700
Db 5641 GTGTAGCACTCTACAGTCCAGGAGCTGAGCAGCTGATGATACCCAGATCCCCACA 5700
Qy 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

RESULT 7

US-09-074-476-1
; Sequence 1, Application US/09074476
; Patent No. 6130322
; GENERAL INFORMATION:
; APPLICANT: Murphy, Patricia D.
; APPLICANT: Allen, Antonette C.
; APPLICANT: Alvares, Christopher P.
; APPLICANT: Critz, Brenda S.
; APPLICANT: Olson, Sheri J.
; APPLICANT: Thurber, Denise
; APPLICANT: Zeng, Bin
; TITLE OF INVENTION: Coding Sequences of the Human
; TITLE OF INVENTION: BRCA1 Gene
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue N. W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

Qy	3901	TATCAATTGAAGAATAGCTTAAATGACATGCGAGTAACCAAGTAATAATTATGGCAAAGGCATCTC	3960
Db	3901	TATCAATTGAAGNATAGCTTAAATGACATGCGAGTAACCAAGGTAATAATTATGGCAAAGGCATCTC	3960
Qy	3961	AGGAACATCACTTAGTCAGGAAACAAANATGTTCTGTAGCTGTGTTTCTTCACATGGCA	4020
Db	3961	AGGAACATCACTTAGTCAGGAAACAAANATGTTCTGTAGCTGTGTTTCTTCACATGGCA	4020
Qy	4021	GTGAATTTGGGAAGACTTGACTGCAAATACAAACACCCAGGATCCCTTTCTTGATTTGGTTCTT	4080
Db	4021	GTGAATTTGGGAAGA CTTGACTGCAAAATACAAACACCCAGGATCCTTTCTTGATTTGGTTCTT	4080
Qy	4081	CCAAA CHAATTCAGGCATCACTCTGTAAAGCCAGGAGTTGGCTGAGTGCACAAAGGAATGG	4140
Db	4081	CCAAA CHAATTCAGGCATCACTCTGTAAAGCCAGGAGTTGGCTGAGTGCACAAAGGAATGG	4140
Qy	4141	TTTCAGATGATGAAGAAAGAGGAACGGGCTTTGGAAGAAAATAATCAAGAAAGACCAAGCA	4200
Db	4141	TTTCAGATGATGAAGAAAGAGGAACGGGCTTTGGAAGAAAATAATCAAGAAAGACCAAGCA	4200
Qy	4201	TGGATTCAAACTTAGGTGAGCAGCATCTCGGTGTGAGAGTGTGAACCAAGCGTCTCTGTAAG	4260
Db	4201	TGGATTCAAACTTAGGTGAGCAGCATCTCGGTGTGAGAGTGTGAACCAAGCGTCTCTGTAAG	4260
Qy	4261	ACTGCTCAGGGCTATCCTCTCAGAGTGCACTTTTAA CCACTCAGCAGAGGGATACCAATGC	4320
Db	4261	ACTGCTCAGGGCTATCCTCTCAGAGTGCACTTTTAA CCACTCAGCAGAGGGATACCAATGC	4320
Qy	4321	AACATACCTCTGATAAAGCTCCAGCAGAGAAATGGCTGAACTTAGAAGCTGTGTAGAACAGC	4380
Db	4321	AACATACCTCTGATAAAGCTCCAGCAGAGAAATGGCTGAACTTAGAAGCTGTGTAGAACAGC	4380
Qy	4381	ATGGAGGCCAGCCCTTTAA CAGCTTAC CCTTCCATPATAAGTGA CTCTTCTGCCCCCTTGAGG	4440
Db	4381	ATGGAGGCCAGCCCTTTAA CAGCTTAC CCTTCCATPATAAGTGA CTCTTCTGCCCCCTTGAGG	4440
Qy	4441	ACCTGCCAAATCCAGAACAAAGACATCAGAAAAAGCAGTATTAACTTTCACAGAAAGTA	4500
Db	4441	ACCTGCCAAATCCAGAACAAAGACATCAGAAAAAGCAGTATTAACTTTCACAGAAAGTA	4500
Qy	4501	GTGAATACCCCTATAAGCCAGAAATCCAGAGGCCCTTTCTGCTGACAAAGTTTGAAGGTGTCG	4560
Db	4501	GTGAATACCCCTATAAGCCAGAAATCCAGAGGCCCTTTCTGCTGACAAAGTTTGAAGGTGTCG	4560
Qy	4561	CAGATAGTCTTACCAGTAAAAATAAGAAACAGGAGTGGAAAGGTCACTCCCTTCTTAAAT	4620
Db	4561	CAGATAGTCTTACCAGTAAAAATAAGAAACAGGAGTGGAAAGGTCACTCCCTTCTTAAAT	4620
Qy	4621	GCCCATCAATTAGATGATGTGTTA CAGTGTGCTCTGCGAGGTCTTCAGANTAGAA	4680
Db	4621	GCCCATCAATTAGATGATGTGTTA CAGTGTGCTCTGCGAGGTCTTCAGANTAGAA	4680
Qy	4681	ACTACCCATCTCAAGAGGAGCTCAATTAAGGTTGTTGATGTGGAGGAGCAACAGCTGGAAAG	4740
Db	4681	ACTACCCATCTCAAGAGGAGCTCAATTAAGGTTGTTGATGTGGAGGAGCAACAGCTGGAAAG	4740
Qy	4741	AGTCTGGGCCACAGATTTGAGCGGAACATCTTACTTGGCCAGCGCAGATCTAGAGGAA	4800
Db	4741	AGTCTGGGCCACAGATTTGAGCGGAACATCTTACTTGGCCAGCGCAGATCTAGAGGAA	4800
Qy	4801	CCCCTTACCTGGAACTCTGGAATCAGCCTCTTCTCTGATGACCCCTGGAATCTGATCCTTCTG	4860
Db	4801	CCCCTTACCTGGAACTCTGGAATCAGCCTCTTCTCTGATGACCCCTGGAATCTGATCCTTCTG	4860
Qy	4861	AAGACAGAGCCCCAGATGCTGTTGTGGCAACATACCACTTCTTCAACCTCTGCATTGA	4920
Db	4861	AAGACAGAGCCCCAGATGCTGTTGTGGCAACATACCACTTCTTCAACCTCTGCATTGA	4920
Qy	4921	AAGTTTCCCCTAATTGAAAGTTTCAGAACTCTGCCAGGGTCCAGCTGCTGTCTCATACTCTG	4980
Db	4921	AAGTTTCCCCTAATTGAAAGTTTCAGAACTCTGCCAGGGTCCAGCTGCTGTCTCATACTCTG	4980

[illegible]

RESULT 8
US-10-022-819-1

; PARENT NO: 6688163
; GENERAL INFORMATION:
: APPLICANT: ALLEN, Antonette C. P.

; RABIN, Mark B.
 TITLE OF INVENTION: CODING SEQUENCE HAPLOTYPE OF THE HUMAN
 ; BRCA1 GENE
 ;

ADDRESSEE: Morgan Lewis & Bockius LLP
STREET: 1111 Pennsylvania Avenue
CITY: Washington DC
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/022,819
  FILING DATE: 22-Apr-2002
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 09/074,452
  FILING DATE: 1998-05-06
ATTORNEY/AGENT INFORMATION:
  NAME: <Unknown>
  REGISTRATION NUMBER: <Unknown>
  REFERENCE/DOCKET NUMBER: 044921-5049-01-US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 202-739-3000
  TELEFAX: 202-739-3001
INFORMATION FOR SEQ ID NO: 1:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 5711 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
    MOLECULE TYPE: DNA (genomic)
    HYPOTHETICAL: NO
    ANTI-SENSE: NO
    FRAGMENT TYPE: N-terminal
  ORIGINAL SOURCE:
    ORGANISM: HOMO SAPIENS
    STRAIN: BRCA1
    HAPLOTYPE: OM14
  POSITION IN GENOME:
    CHROMOSOME/SEGMENT: 17
    MAP POSITION: 17q21
  SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-022-819-1

Query Match      99.9%; Score 5707.8; DB 4; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5709; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGCTCGCTGAGACTTCTCGGACCCCGCAGGCTGTGGGGTTTCTCAGATAACTGGGCC 60
DB 1 AGCTCGCTGAGACTTCTCGGACCCCGCAGGCTGTGGGGTTTCTCAGATAACTGGGCC 60
QY 61 CTGCGCTCAGGAGGCTTCCACCTCTGCTCTGGGTTAAAGTTTCATTGGAAACAGAAAGAAA 120
DB 61 CTGCGCTCAGGAGGCTTCCACCTCTGCTCTGGGTTAAAGTTTCATTGGAAACAGAAAGAAA 120
QY 121 TGGATTATCTCTCTTCGCGTTGAAGAGTACAAAATGTCAATTAATGCTATGCAAGAAA 180
DB 121 TGGATTATCTCTCTTCGCGTTGAAGAGTACAAAATGTCAATTAATGCTATGCAAGAAA 180
QY 181 TCTTAGAGTGTCCCATCTCTGCGTTGAGAGTGTATCAAGGACCTGCTCCACAAAGTGTGACC 240
DB 181 TCTTAGAGTGTCCCATCTCTGCGTTGAGAGTGTATCAAGGACCTGCTCCACAAAGTGTGACC 240
QY 241 ACATATTTTGCAGAAATTTTGCATGCTGAACTTCTCAACAGAGAAAGGGCTTCCACAGT 300
DB 241 ACATATTTTGCAGAAATTTTGCATGCTGAACTTCTCAACAGAGAAAGGGCTTCCACAGT 300
QY 301 GTCCCTTATGTGAAGATGTATTAACCAAGAGGCTTACAGAAAGTACGAGATTATGTC 360
DB 301 GTCCCTTATGTGAAGATGTATTAACCAAGAGGCTTACAGAAAGTACGAGATTATGTC 360
QY 361 AACTTGTTCAGAGCTATTGAAAATCATTTTGTGCTTTTCAGCTTCACACAGGTTTGGAGT 420
DB 361 AACTTGTTCAGAGCTATTGAAAATCATTTTGTGCTTTTCAGCTTCACACAGGTTTGGAGT 420
QY 421 ATGCAACAGCTATATTTTGCAGAAAGGAAATAAATCTCTCTGAAATCTCTAAAGATG 480
DB 421 ATGCAACAGCTATATTTTGCAGAAAGGAAATAAATCTCTCTGAAATCTCTAAAGATG 480
QY 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAACCGTGCACAAAGACTTCTACAGAGTG 540
DB 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAACCGTGCACAAAGACTTCTACAGAGTG 540
QY 541 AACCCGAAATTCCTTCTCTGAGGAAACCAAGTCTCAGTGTCCAACTCTCTAAACCTTGGAA 600
DB 541 AACCCGAAATTCCTTCTCTGAGGAAACCAAGTCTCAGTGTCCAACTCTCTAAACCTTGGAA 600
QY 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATCAAACTCAAAAGACCTCTGTCTACATTTG 660
DB 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATCAAACTCAAAAGACCTCTGTCTACATTTG 660
QY 661 AATTTGGGATCTGATTTCTTGAAGATACCGTTAATAAGGCAACTTATTGAGTGTGGAG 720
DB 661 AATTTGGGATCTGATTTCTTGAAGATACCGTTAATAAGGCAACTTATTGAGTGTGGAG 720
QY 721 ATCAAGAAATTTTACAAATCAACCCCTCAAGAAACCGGATGAATCAGTTTGGATTTCTG 780
DB 721 ATCAAGAAATTTTACAAATCAACCCCTCAAGAAACCGGATGAATCAGTTTGGATTTCTG 780
QY 781 CAAAAGAGGCTGCTTGTGAATTTTCTGAGCGGATGTAAACAAATCTGAACTCATCAAC 840
DB 781 CAAAAGAGGCTGCTTGTGAATTTTCTGAGCGGATGTAAACAAATCTGAACTCATCAAC 840
QY 841 CCAGTAAATGATTTTGAACCACTGAGAAAGCTGCGCTGAGAGCATCCAGAAAGT 900
DB 841 CCAGTAAATGATTTTGAACCACTGAGAAAGCTGCGCTGAGAGCATCCAGAAAGT 900
QY 901 ATCAGGCTAGTCTGTTTCAAACTGAGTGTGGAGCATATGGGCACAAATCTCATGCCA 960
DB 901 ATCAGGCTAGTCTGTTTCAAACTGAGTGTGGAGCATATGGGCACAAATCTCATGCCA 960
QY 961 GCTCATTTACAGCATGAGAAACAGCAGTTTATTACTCACTTAAAGACAGAAATGAATCTAGAAA 1020
DB 961 GCTCATTTACAGCATGAGAAACAGCAGTTTATTACTCACTTAAAGACAGAAATGAATCTAGAAA 1020
QY 1021 AGGCTGAATTTCTGTAATAAAGCAACAGCTGTGCTTAGCAAGGAGCAACATAACAGAT 1080
DB 1021 AGGCTGAATTTCTGTAATAAAGCAACAGCTGTGCTTAGCAAGGAGCAACATAACAGAT 1080
QY 1081 GGGCTGGAAGTAAAGGAAACATGTAATCATAGGCGGACTCCAGCACAGAAAAAGGTAG 1140
DB 1081 GGGCTGGAAGTAAAGGAAACATGTAATCATAGGCGGACTCCAGCACAGAAAAAGGTAG 1140
QY 1141 ATCTGAATGCTGATPCCCTCTGTGAGAGAAAGAAATGGAATPAAGCAAAACTGCTGCT 1200
DB 1141 ATCTGAATGCTGATPCCCTCTGTGAGAGAAAGAAATGGAATPAAGCAAAACTGCTGCT 1200
QY 1201 CAGAGAACTCTAGAGATCTGAGATGTTCTCTTGGATTAACACTAAATAGCAGCATTCAGA 1260
DB 1201 CAGAGAACTCTAGAGATCTGAGATGTTCTCTTGGATTAACACTAAATAGCAGCATTCAGA 1260
QY 1261 AAGTTAATGAGTGGTTTTTCCAGAAAGTATGAACTGTTAGTGTCTGATGACTCAGATGATG 1320
DB 1261 AAGTTAATGAGTGGTTTTTCCAGAAAGTATGAACTGTTAGTGTCTGATGACTCAGATGATG 1320
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTACTGATGTATTTGGAGCTTCTAAATGAGGTAGTG 1380
DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTACTGATGTATTTGGAGCTTCTAAATGAGGTAGTG 1380
QY 1381 AATATTCTGGTTCTTTCAGAGAAATAGACTTATCTGGCGCAGTGTCTCATGAGGCTTTAA 1440
DB 1381 AATATTCTGGTTCTTTCAGAGAAATAGACTTATCTGGCGCAGTGTCTCATGAGGCTTTAA 1440
QY 1441 TATCTAAAGTGAAGAGTTTCACTCCAAATCAGTATGAGTGTATATTTGAGAGCAAAATAT 1500
DB 1441 TATCTAAAGTGAAGAGTTTCACTCCAAATCAGTATGAGTGTATATTTGAGAGCAAAATAT 1500
QY 1501 TTGGGAAACCTATTCGGAAGAGCAAGCCCTCCCAACTTAAAGCCATGTAACTGAAATC 1560
DB 1501 TTGGGAAACCTATTCGGAAGAGCAAGCCCTCCCAACTTAAAGCCATGTAACTGAAATC 1560
```

Qy	1561	TAAATATAGGAGCATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCCACAATA	1620
Db	1561	TAAATATAGGAGCATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCCACAATA	1620
Qy	1621	AAATTAAGCGTAAAGAGAGACCTACATCAGCGCTTTCATCTGAGGATTTTATCAAGAAAG	1680
Db	1621	AAATTAAGCGTAAAGAGAGACCTACATCAGCGCTTTCATCTGAGGATTTTATCAAGAAAG	1680
Qy	1681	CAGATTTGGCAGTTCAAAAGACTCTGGAATGATATAATCCGGGAACCTAACCAAGCGGAGC	1740
Db	1681	CAGATTTGGCAGTTCAAAAGACTCTGGAATGATATAATCCGGGAACCTAACCAAGCGGAGC	1740
Qy	1741	AGAAATGGTCAAGTGAATGATTAATAATAGTGGTCAAGAGATTAATAAATAAAGGATGATT	1800
Db	1741	AGAAATGGTCAAGTGAATGATTAATAATAGTGGTCAAGAGATTAATAAATAAAGGATGATT	1800
Qy	1801	CTAATTCAGATGAGAAAATCTTAACCCATAGAAATCACTGGAAGAAAGATCTGCTTTCA	1860
Db	1801	CTAATTCAGATGAGAAAATCTTAACCCATAGAAATCACTGGAAGAAAGATCTGCTTTCA	1860
Qy	1861	AAACGAAAGTCAAGCTATTAAGCAGCAGTATAAGCAATATGGAATCTCGAATTAATATCC	1920
Db	1861	AAACGAAAGTCAAGCTATTAAGCAGCAGTATAAGCAATATGGAATCTCGAATTAATATCC	1920
Qy	1921	ACAAATTCAAAAGCACCTAAAAGAAATAGCTGAGGAGGAAGTCTTTACACGAGCATATTC	1980
Db	1921	ACAAATTCAAAAGCACCTAAAAGAAATAGCTGAGGAGGAAGTCTTTACACGAGCATATTC	1980
Qy	1981	ATGCGCTTGAATAGTACTAGTCACTAGCAATCTAAGCCACCTTAATGTACTGAATGCAAA	2040
Db	1981	ATGCGCTTGAATAGTACTAGTCACTAGCAATCTAAGCCACCTTAATGTACTGAATGCAAA	2040
Qy	2041	TTGATAGTTGTTCTAGCAGTGAAGAGATAAGAAAAAAGATACAAACAAATGCGAGTCA	2100
Db	2041	TTGATAGTTGTTCTAGCAGTGAAGAGATAAGAAAAAAGATACAAACAAATGCGAGTCA	2100
Qy	2101	GSCACAGAGAAACCTCAACATCTAGGAGGTAAAGAACCTGCAACTGAGCGCAAGAGA	2160
Db	2101	GSCACAGAGAAACCTCAACATCTAGGAGGTAAAGAACCTGCAACTGAGCGCAAGAGA	2160
Qy	2161	GTAACAAGCCAAATGAACACAGACAGTAAAGACATGACAGTGATATCTTCCAGAGCTGA	2220
Db	2161	GTAACAAGCCAAATGAACACAGACAGTAAAGACATGACAGTGATATCTTCCAGAGCTGA	2220
Qy	2221	AGTTAAACAATGACCTGGTCTGTTTCTAAGTGTTCATTAACACAGTGAATTAAGAAAT	2280
Db	2221	AGTTAAACAATGACCTGGTCTGTTTCTAAGTGTTCATTAACACAGTGAATTAAGAAAT	2280
Qy	2281	TTGTCATCTAGCTTCCAGAGAGAAAGAAAGAGAGAACTAGAAAACAGTTAAAGTGT	2340
Db	2281	TTGTCATCTAGCTTCCAGAGAGAAAGAAAGAGAGAACTAGAAAACAGTTAAAGTGT	2340
Qy	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAGAGAAAGGTTTGCAAACTG	2400
Db	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAGAGAAAGGTTTGCAAACTG	2400
Qy	2401	AAAGATCTGTACAGAGTAGCAGTATTTCACTGGTACCTGGTACTGATTTGGCACTCAGG	2460
Db	2401	AAAGATCTGTACAGAGTAGCAGTATTTCACTGGTACCTGGTACTGATTTGGCACTCAGG	2460
Qy	2461	AAAGATCTCTGGTACTGGAAGTTAGCACTCTAGGAGAAAGCAAGAACTAGAAAACAGTTAAAT	2520
Db	2461	AAAGATCTCTGGTACTGGAAGTTAGCACTCTAGGAGAAAGCAAGAACTAGAAAACAGTTAAAT	2520
Qy	2521	GTGTGAGTCACTGTCAGCATTTGAAACCCCAAGGACTAATTCATGGTGTTCCTCAAG	2580
Db	2521	GTGTGAGTCACTGTCAGCATTTGAAACCCCAAGGACTAATTCATGGTGTTCCTCAAG	2580
Qy	2581	ATAATAGAAATGACACAGAAAGCTTTAAGTATCCATTTGGGACATGAAGTTAAACCACTC	2640
Db	2581	ATAATAGAAATGACACAGAAAGCTTTAAGTATCCATTTGGGACATGAAGTTAAACCACTC	2640

Qy	2641	GGGAAACAAGCATAGAAAATGGAAGAGTGAATCTGATCTCAGTATTTTGCAGAAATACAT	2700
Db	2641	GGGAAACAAGCATAGAAAATGGAAGAGTGAATCTGATCTCAGTATTTTGCAGAAATACAT	2700
Qy	2701	TCAGGTTTCAAGCCGAGTCAATTTGCTCTGTTTCAAAATCCAGGAAATGCAAGAGAGG	2760
Db	2701	TCAGGTTTCAAGCCGAGTCAATTTGCTCTGTTTCAAAATCCAGGAAATGCAAGAGAGG	2760
Qy	2761	AATGTGCAACATTTCTCTGCCCCTCTGGGCTCTTAAAGAAAAAAGTCCAAAAGTCACTT	2820
Db	2761	AATGTGCAACATTTCTCTGCCCCTCTGGGCTCTTAAAGAAAAAAGTCCAAAAGTCACTT	2820
Qy	2821	TTGAATGTGAACAAAAGGAGAAATCAAGGAAAGATGAGTCTAATATCAAGCCCTGTAC	2880
Db	2821	TTGAATGTGAACAAAAGGAGAAATCAAGGAAAGATGAGTCTAATATCAAGCCCTGTAC	2880
Qy	2881	AGACAGTTAATATCACTGACGCTTTCTGCTGTTGCTCAGAAAGATAGCCAGTTGATA	2940
Db	2881	AGACAGTTAATATCACTGACGCTTTCTGCTGTTGCTCAGAAAGATAGCCAGTTGATA	2940
Qy	2941	ATGCCAAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGCA	3000
Db	2941	ATGCCAAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGCA	3000
Qy	3001	ACGAAACTGCACTCATTTACTCCAAAATAAACAATGCACTTTTACAAAACCCATATCGTATAC	3060
Db	3001	ACGAAACTGCACTCATTTACTCCAAAATAAACAATGCACTTTTACAAAACCCATATCGTATAC	3060
Qy	3061	CACCACTTTTCCCATCAAGTCTTTTAAACTAATAATGTAAGAAAAAATCTGCTAGAGG	3120
Db	3061	CACCACTTTTCCCATCAAGTCTTTTAAACTAATAATGTAAGAAAAAATCTGCTAGAGG	3120
Qy	3121	AAACCTTTGAGGACATTTCAATGTCACCTGAAAGAGAAATGGGAAATGAGAAATTCCTAA	3180
Db	3121	AAACCTTTGAGGACATTTCAATGTCACCTGAAAGAGAAATGGGAAATGAGAAATTCCTAA	3180
Qy	3181	GTACAGTGAGCACAATTTAGCCGTAAATAACATTAAGAGAAAAATGTTTTAAAGAGCCAGCT	3240
Db	3181	GTACAGTGAGCACAATTTAGCCGTAAATAACATTAAGAGAAAAATGTTTTAAAGAGCCAGCT	3240
Qy	3241	CAGCAATATTAATGAAGTAGGTTCCAGTACTTAATGAAGTGGCTCCAGTATTAATGAAA	3300
Db	3241	CAGCAATATTAATGAAGTAGGTTCCAGTACTTAATGAAGTGGCTCCAGTATTAATGAAA	3300
Qy	3301	TAGTTCCTCAGTATGAGAAACATTTCAAGCAGAACTAGGTAGAAAACAGAGGGCCAAAATGA	3360
Db	3301	TAGTTCCTCAGTATGAGAAACATTTCAAGCAGAACTAGGTAGAAAACAGAGGGCCAAAATGA	3360
Qy	3361	ATGCTATCTGTAGATTTAGGAGGTTTSCAAGCTGAGTCTATAACAAAGTCTTCTCTGAA	3420
Db	3361	ATGCTATCTGTAGATTTAGGAGGTTTSCAAGCTGAGTCTATAACAAAGTCTTCTCTGAA	3420
Qy	3421	GTAATTCGAAGCATCTGAAATAAAAAAGCAAGAAATGAAGAGTAGTTTCAAGCTGTTA	3480
Db	3421	GTAATTCGAAGCATCTGAAATAAAAAAGCAAGAAATGAAGAGTAGTTTCAAGCTGTTA	3480
Qy	3481	ATACAGATTTCTCTCCTATCTGATTTTCAGATTAATTTAGAACAGCTATGGAGTAGTC	3540
Db	3481	ATACAGATTTCTCTCCTATCTGATTTTCAGATTAATTTAGAACAGCTATGGAGTAGTC	3540
Qy	3541	ATGCACTCTCAGGTTTGTCTGAGACACTGATGACCTGTTTAGATGATGAGTGAATAAGG	3600
Db	3541	ATGCACTCTCAGGTTTGTCTGAGACACTGATGACCTGTTTAGATGATGAGTGAATAAGG	3600
Qy	3601	AAGTACTAGTTTGTGGAATAATGACATTAAGGAAAGTCTGCTGTTTTTGTAGCAAAAAGCG	3660
Db	3601	AAGTACTAGTTTGTGGAATAATGACATTAAGGAAAGTCTGCTGTTTTTGTAGCAAAAAGCG	3660
Qy	3661	TCCAGAGAGGAGACTTAGCAGGAGTCTTAGCCCTTTTCCATACACATTTGGCTCAGG	3720
Db	3661	TCCAGAGAGGAGACTTAGCAGGAGTCTTAGCCCTTTTCCATACACATTTGGCTCAGG	3720
Qy	3721	GTTAACGAAGAGGGGCCAAGAAATTAGAGTCTCTCAGAAAGAGAACTTATCTAGTGAAGATG	3780

APPLICANT: Schelter, Denise B.
APPLICANT: Zeng, Bin
TITLE OF INVENTION: Coding Sequences of the Human
TITLE OF INVENTION: BRCA1 Gene
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: ONCORMED
STREET: 200 Perry Parkway
CITY: Gaithersburg
STATE: MD
COUNTRY: USA
ZIP: 20877
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,691
FILING DATE: 12-Feb-97
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Thomas Gallegos
REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: PA-0054CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-527-2051
TELEFAX: 301-208-6997
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCA1
POSITION IN GENOME: 17
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
US-08-798-691-3

Query Match 99.9%; Score 5703; DB 1; Length 5711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5706; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 AGCTGCTGAGACTTCCTGGACCCCGCACAGGCTGTGGGGTTCTCAGATAACTGGGCC 60
DB 1 AGCTGCTGAGACTTCCTGGACCCCGCACAGGCTGTGGGGTTCTCAGATAACTGGGCC 60
QY 61 CTGCGCTCAGAGGCTTCACCCCTGCTCTGGGTAAAGTTTCATTTGGAACAGAAAGAAA 120
DB 61 CTGCGCTCAGAGGCTTCACCCCTGCTCTGGGTAAAGTTTCATTTGGAACAGAAAGAAA 120
QY 121 TGGATTATCTGCTCTTCGGGTGAAGAGTACAAATGCTATTAATGCTATGCGAGAAA 180
DB 121 TGGATTATCTGCTCTTCGGGTGAAGAGTACAAATGCTATTAATGCTATGCGAGAAA 180
QY 181 TCTTAGAGTGTCCCATCTCTCTGGAGTTGATCAAGGAACCTGTCTCCAAAGTGTGACC 240
DB 181 TCTTAGAGTGTCCCATCTCTCTGGAGTTGATCAAGGAACCTGTCTCCAAAGTGTGACC 240
QY 241 ACNATTTTGCATTTTTCGATGCTGAACCTTCTCAACAGAGAAAGGGCTTCACAGT 300
DB 241 ACNATTTTGCATTTTTCGATGCTGAACCTTCTCAACAGAGAAAGGGCTTCACAGT 300
QY 301 GTCCCTTATGTAAGATGATATAACCAAGAGGAGCTCAAGAAAGTACGAGATTTAGTC 360
DB 301 GTCCCTTATGTAAGATGATATAACCAAGAGGAGCTCAAGAAAGTACGAGATTTAGTC 360
QY 361 AACTTGTGAAGAGCTATTGAAAATCATTTTGTGCTTTTTCAGCTTGACACAGGTTGGAGT 420
DB AACTTGTGAAGAGCTATTGAAAATCATTTTGTGCTTTTTCAGCTTGACACAGGTTGGAGT 420

DB AACTTGTGAAGAGCTATTGAAAATCATTTTGTGCTTTTTCAGCTTGACACAGGTTGGAGT 420
QY 421 ATCCAAACAGCTATAATTTTGGCAAAAAGAAAATACTCTCTGTAACATCTTAAAGATG 480
DB ATCCAAACAGCTATAATTTTGGCAAAAAGAAAATACTCTCTGTAACATCTTAAAGATG 480
QY 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACGCTGCCAAAAGACTTCTACAGAGT 540
DB AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACGCTGCCAAAAGACTTCTACAGAGT 540
QY 541 AACCCGAAAATCTTCTCTGCGAGAAACAGTCTCAGTGTCCAACTCTCTTAACTCTTGAA 600
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QY 601 CTGTGGAACCTCTGAGGACAAACAGCGGTATACCACTCAAAAGAGCTGTCTTACATG 660
DB CTGTGGAACCTCTGAGGACAAACAGCGGTATACCACTCAAAAGAGCTGTCTTACATG 660
QY 661 AATTGGGATCTGATTTCTTGAAGTACCGTTAATAAGCAACTTATGCAAGTGTGGAG 720
DB AATTGGGATCTGATTTCTTGAAGTACCGTTAATAAGCAACTTATGCAAGTGTGGAG 720
QY 721 ATCAAGAAATTTTACAAATCAACCCCTCAGGAACCGAGGATGAATCAGTTTGTGAT 780
DB ATCAAGAAATTTTACAAATCAACCCCTCAGGAACCGAGGATGAATCAGTTTGTGAT 780
QY 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGACGGATGTAAACAAATCTGAAACATCATCAAC 840
DB CAAAAAAGGCTGCTTGTGAATTTTCTGAGACGGATGTAAACAAATCTGAAACATCATCAAC 840
QY 841 CCAGTAATATGATTGAAACACCACTGAGAGCGGTGAGCTGAGAGGATCCAGAAAGT 900
DB CCAGTAATATGATTGAAACACCACTGAGAGCGGTGAGCTGAGAGGATCCAGAAAGT 900
QY 901 ATCAGGGTAGTTCTGTTTCAAACTTGTGATGAGCCATGTGGCAAAATCTCATGCA 960
DB ATCAGGGTAGTTCTGTTTCAAACTTGTGATGAGCCATGTGGCAAAATCTCATGCA 960
QY 961 GCTCATTACAGATGAGAAACAGAGTTTATCTCCTAAAGACAGAAATGATGTAGAAA 1020
DB GCTCATTACAGATGAGAAACAGAGTTTATCTCCTAAAGACAGAAATGATGTAGAAA 1020
QY 1081 GGGCTGGAAGTAAAGAAACATGTAAATCATAGGCGGATCCAGACAGAAAGGATG 1140
DB GGGCTGGAAGTAAAGAAACATGTAAATCATAGGCGGATCCAGACAGAAAGGATG 1140
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATGGAATGAGAACTGCTGCT 1200
DB ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATGGAATGAGAACTGCTGCT 1200
QY 1201 CAGAGATCTCTAGAGATATCTGAAGATGTTCTTGGATAACACTAAATAGCAGCATTCAGA 1260
DB CAGAGATCTCTAGAGATATCTGAAGATGTTCTTGGATAACACTAAATAGCAGCATTCAGA 1260
QY 1261 AAGTTATGATGTTGTTTTCAGAAAGTATGAACTGTAGTTCTGATGATCTCATCATGATG 1320
DB AAGTTATGATGTTGTTTTCAGAAAGTATGAACTGTAGTTCTGATGATCTCATCATGATG 1320
QY 1321 GGGAGTCTGAATCAATGCAAGTAGCTGATGATTTGGAGCTTCTAAATCAGGCTAGATG 1380
DB GGGAGTCTGAATCAATGCAAGTAGCTGATGATTTGGAGCTTCTAAATCAGGCTAGATG 1380
QY 1381 AATATCTGTTTCTCAGAGAAATATAGCTTCTGCGCAGTGATCTCTCATGAGGCTTTAA 1440
DB AATATCTGTTTCTCAGAGAAATATAGCTTCTGCGCAGTGATCTCTCATGAGGCTTTAA 1440
QY 1441 TATCTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAAATATTGAAGACAAAAAT 1500
DB TATCTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAAATATTGAAGACAAAAAT 1500

Qy	1501	TTGGGAAAACCTATCGAAGAGCGAAGCCTCCCAAATTAGCCCATGTAATCTGAATAATC	1560
Db	1501	TTGGGAAAACCTATCGAAGAGCGAAGCCTCCCAAATTAGCCCATGTAATCTGAATAATC	1560
Qy	1561	TAATTTAGAGGCAATTTGTTACTGAGCCACAGATTAACAGAGCGTCCCTCCACAAATA	1620
Db	1561	TAATTTAGAGGCAATTTGTTACTGAGCCACAGATTAACAGAGCGTCCCTCCACAAATA	1620
Qy	1621	AAITAAAGCGTAAAGAGGAGACCTACATCAGGCGCTTCATCTCAGGAGTTTATCAAGAAAG	1680
Db	1621	AAITAAAGCGTAAAGAGGAGACCTACATCAGGCGCTTCATCTCAGGAGTTTATCAAGAAAG	1680
Qy	1681	CAGATTGGCAGTTCAAAGAGCTCTGAAATGATTAATCAGGGAACTTAACCAAACGGAGC	1740
Db	1681	CAGATTGGCAGTTCAAAGAGCTCTGAAATGATTAATCAGGGAACTTAACCAAACGGAGC	1740
Qy	1741	AGAATGCTCAAGTGATGAATATTACTAAATAGTGGTCTATGAGAAATAAAACAAAGGTGATT	1800
Db	1741	AGAATGCTCAAGTGATGAATATTACTAAATAGTGGTCTATGAGAAATAAAACAAAGGTGATT	1800
Qy	1801	CTATTCAAGATGAGAAAATCTTAACCCCAATAGATCACTCGAAAAAGAAATCTGCTTTCA	1860
Db	1801	CTATTCAAGATGAGAAAATCTTAACCCCAATAGATCACTCGAAAAAGAAATCTGCTTTCA	1860
Qy	1861	AAACGAAGCTGAACCTTATAGCAGCAGTATAGCAATATGAACTCGAAATTAATATACC	1920
Db	1861	AAACGAAGCTGAACCTTATAGCAGCAGTATAGCAATATGAACTCGAAATTAATATACC	1920
Qy	1921	ACAAATCAAAGCACTTAAGAGAAATAGGCTCGAGGAGAAATCTTACCAAGCAATATTC	1980
Db	1921	ACAAATCAAAGCACTTAAGAGAAATAGGCTCGAGGAGAAATCTTACCAAGCAATATTC	1980
Qy	1981	ATGGCTTGAACTAGTAGTCAGTAAATCTAAGCCCACTAAATGTTACTGATGCAAA	2040
Db	1981	ATGGCTTGAACTAGTAGTCAGTAAATCTAAGCCCACTAAATGTTACTGATGCAAA	2040
Qy	2041	TTGATAGTCTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACAAATGCGAGTCA	2100
Db	2041	TTGATAGTCTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACAAATGCGAGTCA	2100
Qy	2101	GGCAGCAGAAACCTCAAACTCATGGAGGTAAGAACTCGCAATCTGGAGCCAAAGAGA	2160
Db	2101	GGCAGCAGAAACCTCAAACTCATGGAGGTAAGAACTCGCAATCTGGAGCCAAAGAGA	2160
Qy	2161	GTAACAGCCAAATGAACAGCAAGTAAAGACATGACAGTGTATCTTTCCAGAGCTGA	2220
Db	2161	GTAACAGCCAAATGAACAGCAAGTAAAGACATGACAGTGTATCTTTCCAGAGCTGA	2220
Qy	2221	AGTTAAACAAATGCACCTGGTCTTTTACTAAGTGTCAAATACCACTGAACTTAAAGAA	2280
Db	2221	AGTTAAACAAATGCACCTGGTCTTTTACTAAGTGTCAAATACCACTGAACTTAAAGAA	2280
Qy	2281	TTGTCAATCTAGCTTCCAGAGAGAGAAAGAGAGAGAACTAGAAACAGTTAAGTGT	2340
Db	2281	TTGTCAATCTAGCTTCCAGAGAGAGAAAGAGAGAGAACTAGAAACAGTTAAGTGT	2340
Qy	2341	CTAATAATGCTGAAGACCCCAAAGATCTCATGTTTAAGTCGAGAAAGGGTTTTGCAAACTG	2400
Db	2341	CTAATAATGCTGAAGACCCCAAAGATCTCATGTTTAAGTCGAGAAAGGGTTTTGCAAACTG	2400
Qy	2401	AAAGATCTGTAGAGAGTAGCAGTATTTTCACTGGTACTGCTGATGATGCACTCAGG	2460
Db	2401	AAAGATCTGTAGAGAGTAGCAGTATTTTCACTGGTACTGCTGATGATGCACTCAGG	2460
Qy	2461	AAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGCCAAAAACAGAACTAAT	2520
Db	2461	AAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGCCAAAAACAGAACTAAT	2520
Qy	2521	GTFGAGTCAAGTGTGAGGATTTTGAAGAACCCAGAGGACTAATTCATGGTGTCCCAAG	2580
Db	2521	GTFGAGTCAAGTGTGAGGATTTTGAAGAACCCAGAGGACTAATTCATGGTGTTCCTCAAG	2580
Qy	2581	ATAATAGAAATGACACAGAGAGCTTTTAAGTATCATTTGGGACATGAAGTTAAACCAAGTC	2640
Db	2581	ATAATAGAAATGACACAGAGAGCTTTTAAGTATCATTTGGGACATGAAGTTAAACCAAGTC	2640
Qy	2641	GGGAAACAAGCANTAGAAATGGAAGAGTGAACCTTGATGCTCAGTATTTGCAGAAATACAT	2700
Db	2641	GGGAAACAAGCANTAGAAATGGAAGAGTGAACCTTGATGCTCAGTATTTGCAGAAATACAT	2700
Qy	2701	TCAAGGTTTCAAAGCGCAGTCAATTTGCTCTGTTTTCAAATCCAGGAAATGCAGAAAGG	2760
Db	2701	TCAAGGTTTCAAAGCGCAGTCAATTTGCTCTGTTTTCAAATCCAGGAAATGCAGAAAGG	2760
Qy	2761	AATGTGCAACATTTCTCTGCCACTCTGGTCTCTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Db	2761	AATGTGCAACATTTCTCTGCCACTCTGGTCTCTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Qy	2821	TTGAATGTGAACAAAGGAAGAAATCAAGGAAAGAAATGAGTCTTAATATCAAGCCTGTAC	2880
Db	2821	TTGAATGTGAACAAAGGAAGAAATCAAGGAAAGAAATGAGTCTTAATATCAAGCCTGTAC	2880
Qy	2881	AGACAGTTTAATATCACTCGAGCTTTCTCTGTTTTGTTGTCATCATCTCAGTTCAGAGGCA	2940
Db	2881	AGACAGTTTAATATCACTCGAGCTTTCTCTGTTTTGTTGTCATCATCTCAGTTCAGAGGCA	2940
Qy	2941	ATGCCAAATGTAAGTATCAAGAGAGCTCTAGGTTTTTGTCTATCATCTCAGTTCAGAGGCA	3000
Db	2941	ATGCCAAATGTAAGTATCAAGAGAGCTCTAGGTTTTTGTCTATCATCTCAGTTCAGAGGCA	3000
Qy	3001	AGAAATCTGGACTCATTTACTCCAATAACATGCACTTTTACAAACCCCATATCGTATAC	3060
Db	3001	AGAAATCTGGACTCATTTACTCCAATAACATGCACTTTTACAAACCCCATATCGTATAC	3060
Qy	3061	CAACACTTTTCCCATCAAGTCAATTTGTTTAAATCTAATGTAAAGAAATCTGCTAGAGG	3120
Db	3061	CAACACTTTTCCCATCAAGTCAATTTGTTTAAATCTAATGTAAAGAAATCTGCTAGAGG	3120
Qy	3121	AAAACCTTTGAGGAAACATTCATGTCACTGAAAGAGAAATGGGAAATGAGAACTTCAA	3180
Db	3121	AAAACCTTTGAGGAAACATTCATGTCACTGAAAGAGAAATGGGAAATGAGAACTTCAA	3180
Qy	3181	GTACAGTGAACAATTTAGCCGTAATAACATTTAGAGAAATTTTAAAGAGCCAGCT	3240
Db	3181	GTACAGTGAACAATTTAGCCGTAATAACATTTAGAGAAATTTTAAAGAGCCAGCT	3240
Qy	3241	CAAGCAATAATTAAGAGTAGTCTCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
Db	3241	CAAGCAATAATTAAGAGTAGTCTCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
Qy	3301	TAGGTTCCAGTCAATGAACATTTCAAGCAGAACTTAGGTAAGAAACAGAGGGCCAAATTTGA	3360
Db	3301	TAGGTTCCAGTCAATGAACATTTCAAGCAGAACTTAGGTAAGAAACAGAGGGCCAAATTTGA	3360
Qy	3361	ATGCTATGCTTAGATTAGGGTTTTGCAACCTGAGGCTCTATAAACAAGTCTCTCTGAAA	3420
Db	3361	ATGCTATGCTTAGATTAGGGTTTTGCAACCTGAGGCTCTATAAACAAGTCTCTCTGAAA	

[illegible]

Db	4741	AGTCTGGGCCACAGGATTTGACGGAAACATCTTACTTGGCCAGCGCAAGATCTAGAGGGAA	4800
Qy	4801	CCCCTTACCTGGGAATCTGGGAATCAGGCTCTTCTCTGATGACCCCTGGAATCTGATCTCTG	4860
Db	4801	CCCCTTACCTGGGAATCTGGGAATCAGGCTCTTCTCTGATGACCCCTGGAATCTGATCTCTG	4860
Qy	4861	AAGACAGAGCCCCAGAGTGCAGCTCTGTCTGGCAACATACCATCTTCAACCTCTGCATTGA	4920
Db	4861	ARGACAGAGCCCCAGAGTGCAGCTCTGTCTGGCAACATACCATCTTCAACCTCTGCATTGA	4920
Qy	4921	AAGTTTCCCAATTGAAAGTTGCGAATCTGCCCCAGGCTCCAGCTGTGTCTCATCTACTCTG	4980
Db	4921	AAGTTTCCCAATTGAAAGTTGCGAATCTGCCCCAGGCTCCAGCTGTGTCTCATCTACTCTG	4980
Qy	4981	ATACGTCTGGGTATTAATGCAATCGAGAAAGTGTGAGCAGGAGAGACCCAGAATTGCACAG	5040
Db	4981	ATACGTCTGGGTATTAATGCAATCGAGAAAGTGTGAGCAGGAGAGACCCAGAATTGCACAG	5040
Qy	5041	CTTCAACAGAAAGGTCACAAAGAAATGTCCATGTGTGTGTGTGCGCTGACCCCGAGAAG	5100
Db	5041	CTTCAACAGAAAGGTCACAAAGAAATGTCCATGTGTGTGTGTGCGCTGACCCCGAGAAG	5100
Qy	5101	AAATTATGCTCTGTATCAAGTTTGCACAGAAACACACATCATCTTTAACTTAATCTAAATTA	5160
Db	5101	AAATTATGCTCTGTATCAAGTTTGCACAGAAACACACATCATCTTTAACTTAATCTAAATTA	5160
Qy	5161	CTGAAGAGACTACTCATCTTGTATTGAAGAACAGATGCTGAGTTTGTGTGAGACGGACAC	5220
Db	5161	CTGAAGAGACTACTCATCTTGTATTGAAGAACAGATGCTGAGTTTGTGTGAGACGGACAC	5220
Qy	5221	TGAATATTTTCTAGGAATTTCCGGGAGGAAATGSGGTAGTTAGCTATTTCTGGGTGACCC	5280
Db	5221	TGAATATTTTCTAGGAATTTCCGGGAGGAAATGSGGTAGTTAGCTATTTCTGGGTGACCC	5280
Qy	5281	AGTCTATTAAAGAGAPAGAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG	5340
Db	5281	AGTCTATTAAAGAGAGAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG	5340
Qy	5341	TCAATGGAAGAACCCACCAAGGTCCTAAGCGAGCAGAGNATCCCGGACAGAGAAATCT	5400
Db	5341	TCAATGGAAGAACCCACCAAGGTCCTAAGCGAGCAGAGNATCCCGGACAGAGAAATCT	5400
Qy	5401	TCAGGGGGCTAGAAATCTGTTGTCTATGGGCCCTTCCAAACATGCCACAGATCAACTGG	5460
Db	5401	TCAGGGGGCTAGAAATCTGTTGTCTATGGGCCCTTCCAAACATGCCACAGATCAACTGG	5460
Qy	5461	AATGGAATGATACAGCTGTGTGTGCTTCTGTGTGAGAGGACTTTCAFCATTCACCCCTTG	5520
Db	5461	AATGGAATGATACAGCTGTGTGTGCTTCTGTGTGAGAGGACTTTCAFCATTCACCCCTTG	5520
Qy	5521	GCAAGGTGTCCACCCCAATTTGGTTGTGTGAGCCAGATGCTGCAGAGAGCAATATGGCT	5580
Db	5521	GCAAGGTGTCCACCCCAATTTGGTTGTGTGAGCCAGATGCTGCAGAGAGCAATATGGCT	5580
Qy	5581	TCCATGCAATTTGGGCAGATGTGTAGGCACCTGTGTGTGACCCGAGAGTGGGTGTGGACA	5640
Db	5581	TCCATGCAATTTGGGCAGATGTGTAGGCACCTGTGTGTGACCCGAGAGTGGGTGTGGACA	5640
Qy	5641	GTGTAGCACTTCTACCAAGTGCAGAGCTGAGACCTTACCTGATACCCACAGATCCCCCACA	5700
Db	5641	GTGTAGCACTTCTACCAAGTGCAGAGCTGAGACCTTACCTGATACCCACAGATCCCCCACA	5700
Qy	5701	GCACACTACTGA	5711
Db	5701	GCACACTACTGA	5711

RESULT 10
US-08-825-487A-3
; Sequence 3, Application US/088255487A
; Patent No. 6048689
; GENERAL INFORMATION:
; APPLICANT: Murphy, Patricia D.

APPLICANT: White, Marga B.
TITLE OF INVENTION: METHODS FOR IDENTIFYING VARIATIONS IN POLYNUCLEOTIDE SEQUENCE
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue., N.W.
CITY: Washington,
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/825,487A
FILING DATE: 28-Mar-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/060002
FILING DATE: 26-Mar-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 05371.0012.999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8100
TELEFAX: 650-463-8400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCAL
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
US-08-825-487A-3

Query Match 99.9%; Score 5703; DB 3; Length 5711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5706; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	1	AGCTGGCTGAGACTTCTCTGGACCCCGACAGGCTGTGGGGTTCTCAGATAA	CTGGGCC	60
Db	1	AGCTGGCTGAGACTTCTCTGGACCCCGACAGGCTGTGGGGTTCTCAGATAA	CTGGGCC	60
Qy	61	CTGGCGCTCAGAGGCGCTTACCCCTCTGCTGGGTAAGTTCAATGGAA	CAGAAAGAA	120
Db	61	CTGGCGCTCAGAGGCGCTTACCCCTCTGCTGGGTAAGTTCAATGGAA	CAGAAAGAA	120
Qy	121	TGGATTATCTGCTCTTGGGTTGAAGAGTACAAATGTCAATTAATCTATG	CAGAAAA	180
Db	121	TGGATTATCTGCTCTTGGGTTGAAGAGTACAAATGTCAATTAATCTATG	CAGAAAA	180
Qy	181	TCTTAGATGTCCTTCTGCTGAGTTGATCAAGAAACCTGTCTCCAAAGT	GTGACC	240
Db	181	TCTTAGATGTCCTTCTGCTGAGTTGATCAAGAAACCTGTCTCCAAAGT	GTGACC	240
Qy	241	ACATATTTGCAATTTTGCATGCTGAACTTCTCAACACAGAGAAAGGCTT	CACAGT	300
Db	241	ACATATTTGCAATTTTGCATGCTGAACTTCTCAACACAGAGAAAGGCTT	CACAGT	300
Qy	301	GTCTTTATGTAAGATGATATAACCAAAAGAGGCTTACAGAAAGTACGAT	TTAGTC	360
Db	301	GTCTTTATGTAAGATGATATAACCAAAAGAGGCTTACAGAAAGTACGAT	TTAGTC	360

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2161 GTAACAGCCAAATCAACAGACAAGTAAAGACAATGACAGTGATATCTTCCAGAGCTGA 2220
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2461 AAAGATCTGTAGTAGGAGTTAGCAGTCTTAGGAGAGGCAAAAACAGAAACCAATTAAT 2520
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2521 GTGTCAGTGCAGCATTTGAAAACCCCAAGGAGCTAATTCATGTTGTTTCCAAAG 2580
2581 ATATTAAGATGACACAGAGGCTTTAAAGTATCATTTGGACATGAAGTTAAACCAAGTC 2640
2581 ATATTAAGATGACACAGAGGCTTTAAAGTATCATTTGGACATGAAGTTAAACCAAGTC 2640
2641 GGGAAAACAAGCATAGAAAATGGAAAGTGAATCTGATGCTCAGTATTTGCGAATAATCAT 2700
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2701 TCAGGTTTCAAGAGCCAGTCATTTGCTCTGTTTCAATCCAGGAAATGAGAGAGG 2760
2701 TCAGGTTTCAAGAGCCAGTCATTTGCTCTGTTTCAATCCAGGAAATGAGAGAGG 2760
2761 AATGTGCAACATTTCTGCCCCACTCTGGGTCTTTAAAGAAACAAAGTCCAAAAAGTCACCT 2820
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2821 TTGAATGTGAACAAAGGAAGAAATCAGGAAGATGAGTCTATATCAAGCCCTGTAC 2880
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2881 AGACAGTTAATATCACTGCAAGGCTTTCTGTTGTTGTCAGAAAGATAGCCAGTTGATA 2940
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3121 AAAACCTTTGAGGAGCACTCAATGTCACCTGAAAGAAATGGAATAGAAATTCCTCAA 3180
3181 GTACAGTGCACAAATTAGCCGTAATTAACATTAAGAGAAATGTTTAAAGAGCCAGCT 3240
3181 GTACAGTGCACAAATTAGCCGTAATTAACATTAAGAGAAATGTTTAAAGAGCCAGCT 3240
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3301 TAGGTTCCAGTGATGAAAACATTCAGCAGAACTAGGTAGAAAACAGAGGCCCAGAAATTTGA 3360
3301 TAGGTTCCAGTGATGAAAACATTCAGCAGAACTAGGTAGAAAACAGAGGCCCAGAAATTTGA 3360
3361 ATGCTATGCTTAGATTAGGGGTTTGCACCTGAGTCTATTAACAAAGTCTTCTCTGGAA 3420
3361 ATGCTATGCTTAGATTAGGGGTTTGCACCTGAGTCTATTAACAAAGTCTTCTCTGGAA 3420
3421 GTAAATCTTAAGCATCTTGAATTAAGAAACAAATATGAAGAGTAGTTTCAAGTCTGTTA 3480
3421 GTAAATCTTAAGCATCTTGAATTAAGAAACAAATATGAAGAGTAGTTTCAAGTCTGTTA 3480
3481 ATACAGATTTCTCTCCATATCTGATTTAGATAAATCTAGAACAGCCCTATGGAGTAGTC 3540
3481 ATACAGATTTCTCTCCATATCTGATTTAGATAAATCTAGAACAGCCCTATGGAGTAGTC 3540
3541 ATGCACTCAGGTTTGTCTGAGACACCTGATGACCTTTAGATGATGGTGAATTAAGG 3600
3541 ATGCACTCAGGTTTGTCTGAGACACCTGATGACCTTTAGATGATGGTGAATTAAGG 3600
3601 AAGATACAGTGTGCTGAAAATGACATTAAGGAAAGTCTGCTGTTTGTAGCAAAAGCG 3660
3601 AAGATACAGTGTGCTGAAAATGACATTAAGGAAAGTCTGCTGTTTGTAGCAAAAGCG 3660


```
GENERAL INFORMATION:
APPLICANT: Murphy, Patricia D.
APPLICANT: Allen, Antonette C.
APPLICANT: Alvares, Christopher P.
APPLICANT: Critz, Brenda S.
APPLICANT: Olson, Sheri J.
APPLICANT: Thurber, Denise
APPLICANT: Zeng, Bin
TITLE OF INVENTION: Coding Sequences of the Human
TITLE OF INVENTION: BRCA1 Gene
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESS: Howrey & Simon
STREET: 1299 Pennsylvania Avenue N. W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,476
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/074,453
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 5371.34.US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8109
TELEFAX: 650-463-8400
INFORMATION FOR SEQ ID NO. 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCA1 (om13)
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
US-09-074-476-5

Query Match 99.9%; Score 5703; DB 3; Length 5711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5706; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 121 TGGATTTATCTGCTCTTGGGTGAGAGGATACAAATGTCAATTAATCTATGAGAAA 180
QY 181 TCTTAGAGTGCTCCATCTGTCTGGAGTTGATCAAGAAACCTGTCTCCAAAGAGTGTGACC 240
DB 181 TCTTAGAGTGCTCCATCTGTCTGGAGTTGATCAAGAAACCTGTCTCCAAAGAGTGTGACC 240
QY 241 ACATATTTTGCATAATTTTGCATGCTGAAACTTCTCAACAGAGAAAGGCGCTTCACAGT 300

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1141 601 CTGTGAGAACTCTGAGGAAACCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 660
1141 601 CTGTGAGAACTCTGAGGAAACCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 660
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1141 661 AATTGGGATCTGATTCTTCTGAAGATACCCCTTAATTAAGGCAACTTATGAGTGTGGAG 720
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1141 721 ATCAGAAATTTTACAAATCAACCCCTCAAGGAAACCAAGGATGAAATCAGTTTGGATTCTG 780
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1141 901 ATCAGGCTAGTCTGTTTCAAACTTGTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 960
1141 961 GCTCATTACAGCATGAGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1020
1141 961 GCTCATTACAGCATGAGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1020
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1141 1021 AGGCTGAATTTCTGTAATTAAGCAACAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1080
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1141 1141 ATCTGATGCTGATCCCTCTGCTGAGAGGAAAGATGGAATTAAGCAAGAAAGGTTAG 1200
1141 1201 CAGAGAACTCTAGAGATGATGAAAGTGTCTCTTGGATAACACTTAAATAGCAGCATTCAGA 1260
1141 1201 CAGAGAACTCTAGAGATGATGAAAGTGTCTCTTGGATAACACTTAAATAGCAGCATTCAGA 1260
1141 1261 AAGTTAATGATGGTTTCCAGAGGATGAAATCTGTTAGGTTCTGATCTCAGATTCAGT 1320
1141 1261 AAGTTAATGATGGTTTCCAGAGGATGAAATCTGTTAGGTTCTGATCTCAGATTCAGT 1320
1141 1321 GGGAGTCTGAAATCAAAATGCGAAAGTGTGATGATTTTGGAGGCTTCTAAATGAGGTAGATG 1380
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Db 1321 GGGAGTCTGAATCAATGCCAAAGTAGCTGATGTATTTGGACGTTCTAAATGAGGTAGATG 1380
Qy 1381 AATATTTCTGGTCTTTCAGAGAAATAGACTTACTGGCCAGTGATCCTCATGAGGCTTAA 1440
Db 1381 AATATTTCTGGTCTTTCAGAGAAATAGACTTACTGGCCAGTGATCCTCATGAGGCTTAA 1440
Qy 1441 TATGTAAAGGTGAAAGAGTTCACCTCAAATCAGTAGAGAGTAATATTCAGAGCAAAATAT 1500
Db 1441 TATGTAAAGGTGAAAGAGTTCACCTCAAATCAGTAGAGAGTAATATTCAGAGCAAAATAT 1500
Qy 1501 TTGGGAAACCTATTCGGGAAGGAGGAGGCTCCCGAACCTTAAGCGTGTACTGAAATC 1560
Db 1501 TTGGGAAACCTATTCGGGAAGGAGGAGGCTCCCGAACCTTAAGCGTGTACTGAAATC 1560
Qy 1561 TAAATTTATAGGAGCATTTGTACTGAGCCACAGATAATACAAAGAGGCTCCCTCACAATA 1620
Db 1561 TAAATTTATAGGAGCATTTGTACTGAGCCACAGATAATACAAAGAGGCTCCCTCACAATA 1620
Qy 1621 AATTAAGCGTAAAGAGGAGCTACATCAGGCGCTTCATCTCGAGGATTTTATCAAGAAAG 1680
Db 1621 AATTAAGCGTAAAGAGGAGCTACATCAGGCGCTTCATCTCGAGGATTTTATCAAGAAAG 1680
Qy 1681 CAGATTTGGCAGTTCAGAAAGACTCCTGAAATGATAAATCAGGGAAGTAAACCAAGCGAGC 1740
Db 1681 CAGATTTGGCAGTTCAGAAAGACTCCTGAAATGATAAATCAGGGAAGTAAACCAAGCGAGC 1740
Qy 1741 AGAATGGTCAAGTGTGAATATTAATAGTGGTTCATGAGATTAATAAACAAGGTGAT 1800
Db 1741 AGAATGGTCAAGTGTGAATATTAATAGTGGTTCATGAGATTAATAAACAAGGTGAT 1800
Qy 1801 CTATTCAGAAATGAGAAATCCTTAACCAATAGAAATCACTCGAAAGAAATCTGCTTTCA 1860
Db 1801 CTATTCAGAAATGAGAAATCCTTAACCAATAGAAATCACTCGAAAGAAATCTGCTTTCA 1860
Qy 1861 AAACGAAAGCTGAACTATAAGCAGCAGTATAAGCAATATGGAATCGAAATTAATATCC 1920
Db 1861 AAACGAAAGCTGAACTATAAGCAGCAGTATAAGCAATATGGAATCGAAATTAATATCC 1920
Qy 1921 ACAATTCAGAAAGCCTTAAAGAAATAGCTGTAGGAGGAGTCTTCTACAGGCAATATTC 1980
Db 1921 ACAATTCAGAAAGCCTTAAAGAAATAGCTGTAGGAGGAGTCTTCTACAGGCAATATTC 1980
Qy 1981 ATGCGCTTGAATAGTAGTAGTGAATAATCTAAGCCCACTTAATGTACTGAAATGCGAA 2040
Db 1981 ATGCGCTTGAATAGTAGTAGTGAATAATCTAAGCCCACTTAATGTACTGAAATGCGAA 2040
Qy 2041 TTGATAGTGTCTTAGCAGTGAAGATTAAGAAAGAAAGATGACCAATATGCGAGTCA 2100
Db 2041 TTGATAGTGTCTTAGCAGTGAAGATTAAGAAAGAAAGATGACCAATATGCGAGTCA 2100
Qy 2101 GGCAAGCAGAAACCTCAACTCAGGAGGTAAAGACCTGCACTGAGGCCAAGAGA 2160
Db 2101 GGCAAGCAGAAACCTCAACTCAGGAGGTAAAGACCTGCACTGAGGCCAAGAGA 2160
Qy 2161 GTAAAGCAGAAATGAACAGACCAAGTAAAGACATGACAGGTGATATTTCCAGAGCTGA 2220
Db 2161 GTAAAGCAGAAATGAACAGACCAAGTAAAGACATGACAGGTGATATTTCCAGAGCTGA 2220
Qy 2221 AGTTAAAGTGCACCTGGTCTTTTACTAGTGTGTTCAATACCAAGTGAATTTAAAGAAAT 2280
Db 2221 AGTTAAAGTGCACCTGGTCTTTTACTAGTGTGTTCAATACCAAGTGAATTTAAAGAAAT 2280
Qy 2281 TTGTCNAATCCTAGCCTTCCAGAGAGAAAGAAAGAGAAACTAGAAACAGTTAAAGTGT 2340
Db 2281 TTGTCNAATCCTAGCCTTCCAGAGAGAAAGAAAGAGAAACTAGAAACAGTTAAAGTGT 2340
Qy 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAGGTTTTGCAACTG 2400
Db 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAGGTTTTGCAACTG 2400
Qy 2401 AAAGATCTGTAGAGAGTACAGTATTTCACTGGTACCTGGTACTGATTTATGCGACTCAGG 2460
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Qy 2461 AAAGATCTCTGTTACTGGAAAGTTAGCACTCTAGGAAAGGCAAAAACAGAAACCAATAAAT 2520
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Qy 2521 GTGTGAGTCAAGTGTGAGCAATTTGAAAAACCCCAAGGGACTAATTTCTGTTGTTTCCAAG 2580
Db 2521 GTGTGAGTCAAGTGTGAGCAATTTGAAAAACCCCAAGGGACTAATTTCTGTTGTTTCCAAG 2580
Qy 2581 ATAATAGAAATGACACAGAAAGGCTTTAAAGTATCCATTTGGGACATGAAGTTAAACCAAGTC 2640
Db 2581 ATAATAGAAATGACACAGAAAGGCTTTAAAGTATCCATTTGGGACATGAAGTTAAACCAAGTC 2640
Qy 2641 GGGAAAACAAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCGATTTTGCAGAAATCAT 2700
Db 2641 GGGAAAACAAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCGATTTTGCAGAAATCAT 2700
Qy 2701 TCAGGTTTTCAAAAGCGCCAGTCATTTGCTCTGTTTTCAAATCCAGGAAATGCGAGAAAGG 2760
Db 2701 TCAGGTTTTCAAAAGCGCCAGTCATTTGCTCTGTTTTCAAATCCAGGAAATGCGAGAAAGG 2760
Qy 2761 AATGTGCAACATTTCTTGCCCACTCTGGGCTCTTAAAGAAACAAAGTCCAAAAGTCACTT 2820
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Db 2821 TTGNAATGTGAACAAAGGAGAAATCAAGGAAAGATGATCTTAATATCAAGGCTCTGAC 2880
Qy 2881 AGCAGTTAATATCACTGCGAGGCTTTCTGTTGGTTCAGAAAGATGATGATTAATCAAGGCTCTGAC 2940
Db 2881 AGCAGTTAATATCACTGCGAGGCTTTCTGTTGGTTCAGAAAGATGATGATTAATCAAGGCTCTGAC 2940
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Qy 3001 ACAGAACTGCACTCATTTACTTCCAAAATAAACAATGCACTTTTACAAAACCCATATGCTATAC 3060
Db 3001 ACAGAACTGCACTCATTTACTTCCAAAATAAACAATGCACTTTTACAAAACCCATATGCTATAC 3060
Qy 3061 CACACATTTTCCCATCAAGTCATTTGTTAAACTTAAATGTAAGAAATCTGCTAGAGG 3120
Db 3061 CACACATTTTCCCATCAAGTCATTTGTTAAACTTAAATGTAAGAAATCTGCTAGAGG 3120
Qy 3121 AAAAATTTGAGGAGCACTTCAATGTCCTGAAAGAGAAATGGGAAATGAGAAATTCCTCA 3180
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Db 3181 GTACAGTGAAGCAAAATTAGCCGTAATAACATTAGAGAAATGTTTTTAAAGGAGCCAGCT 3240
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Db 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTTAATGAAGTGGGCTCCAGTTAATGAAT 3300
Qy 3301 TAGGTTCCAGTGAATAACATTCAGAGCAAGCTAGGTAGAAACAGAGGGCCAAAATTTGA 3360
Db 3301 TAGGTTCCAGTGAATAACATTCAGAGCAAGCTAGGTAGAAACAGAGGGCCAAAATTTGA 3360
Qy 3361 ATGCTATGCTTAGANTAGGGGTTTTGCAACTGAGGCTCTAATAACAAAGTCTTCTCTGAA 3420
Db 3361 ATGCTATGCTTAGANTAGGGGTTTTGCAACTGAGGCTCTAATAACAAAGTCTTCTCTGAA 3420
Qy 3421 GTAAATGTAAAGCATCTCTGAAATAAAAAGCAAGATATGAAGAGTAGTTTCAAGCTGTTA 3480
Db 3421 GTAAATGTAAAGCATCTCTGAAATAAAAAGCAAGATATGAAGAGTAGTTTCAAGCTGTTA 3480
Qy 3481 ATACAGATTTCTCTCCATATCTGATTTTCAGATTAATTTAGAACAGCTTATGGGAAGTAGTC 3540
Db 3481 ATACAGATTTCTCTCCATATCTGATTTTCAGATTAATTTAGAACAGCTTATGGGAAGTAGTC 3540

Qy	3541	ATGCACTCAGGTTTGTTCTTGAACACCTGATGACCTGTGTAGTAGTGGTGAATAAAGG	3600
Db	3541	ATGCATCTCAGGTTTGTTCTTGAACACCTGATGACCTGTGTAGTAGTGGTGAATAAAGG	3600
Qy	3601	AAGATACTAGTTTTGCTGAAAATTCACATTAAGGAAAGTTCTCGTGTGTTTTTAGCAAAGCG	3660
Db	3601	AAGATACTAGTTTTGCTGAAAATTCACATTAAGGAAAGTTCTCGTGTGTTTTTAGCAAAGCG	3660
Qy	3661	TCCAGAGAGAGACTTTPAGCAGAGTCTTAGGCCCTTTACCCATACACATTTGGCTCAGG	3720
Db	3661	TCCAGAAAGAGAGCTTTPAGCAGAGTCTTAGGCCCTTTACCCATACACATTTGGCTCAGG	3720
Qy	3721	GTTTACCAGAACGGGCCCAAGAAATTAGAGTCTCAGAGAGAACTTATCTAGTGGAGTG	3780
Db	3721	GTTTACCAGAACGGGGCCCAAGAAATTAGAGTCTCAGAGAGAACTTATCTAGTGGAGTG	3780
Qy	3781	AAGAGCTTCCCTGCTTCCACAACCTTGTTATTATTTGGTAAAGTAAACAATATACCTTCTCAGT	3840
Db	3781	AAGAGCTTCCCTGCTTCCACAACCTTGTTATTATTTGGTAAAGTAAACAATATATACCTTCTCAGT	3840
Qy	3841	CTACTAGGCATACGACCGTTGCTACCGAGTGTCTGTCTTAGAACACAGAGGGAATTTAT	3900
Db	3841	CTACTAGGCATACGACCGTTGCTACCGAGTGTCTGTCTTAGAACACAGAGGGAATTTAT	3900
Qy	3901	TATCATTTGAAGAATAGCTTTAAATGACTGCAGTAACACAGGTAAATTGGCAAAGCCATCTC	3960
Db	3901	TATCATTTGAAGATAGCTTTAAATGACTGCAGTAACACAGGTAAATTGGCAAAGCCATCTC	3960
Qy	3961	AGGAACATCACTTPTAGTGAGGAAACAAATATGTTCTGCTAGCTTGTGTTTTCTTACAGTGCA	4020
Db	3961	AGGAACATCACTTPTAGTGAGGAAACAAATATGTTCTGCTAGCTTGTGTTTTCTTACAGTGCA	4020
Qy	4021	GTGAATTTGGAAGACTTCACTGCAATACAAACACCCAGAGTCCCTTCTGTAATGGTTCCT	4080
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Qy	4081	CCAAACAAATGAGGCATCAGTCTGAAAGCCAGGGAGTTGTTCTGAGTGACAGGAAATGG	4140
Db	4081	CCAAACAAATGAGGCATCAGTCTGAAAGCCAGGGAGTTGTTCTGAGTGACAGGAAATGG	4140
Qy	4141	TTTTCAGATGTAGAAAGAGGAAACGGCTTGGNAGAAATATATCAGRAGAGCGCAAGCA	4200
Db	4141	TTTTCAGATGTAGAAAGAGGAAACGGCTTGGNAGAAATATATCAGRAGAGCGCAAGCA	4200
Qy	4201	TGGATTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAACAAGCGTCTCTGAAG	4260
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Qy	4261	ACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAACTCCTCAGCAGAGGGATACCATGC	4320
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Qy	4321	AACATAACCTTGATAAAGCTCCAGCAGCAAAATGGCTGAACTAGAGCTGTGTAGAACAGC	4380
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Qy	4381	ATGGAGCGCAGCCTTTTAAACAGCTACCTTCCATCATATAGTGACTCTTCTGCCCTTGAAG	4440
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Qy	4501	GTGAATACCTTATTAAGCCAGAAATCCAGAGAGCCCTTTCTGCTGACAGTTTGAAGTGCTG	4560
Db	4501	GTGAATACCTTATTAAGCCAGAAATCCAGAGAGCCCTTTCTGCTGACAGTTTGAAGTGCTG	4560
Qy	4561	CAGATAGTTCTTACCAGTATAAATAAGAACACAGAGGTGGAAGGTCAATCCCCTTCTAAAT	4620
Db	4561	CAGATAGTTCTTACCAGTATAAATAAGAACACAGAGGTGGAAGGTCAATCCCCTTCTAAAT	4620
Qy	4621	GCCCATCATTAGATCATAGTGGTGTACATGCAACAGTTGCTCTGGGAGTCTTTCAGAAATGAA	4680

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4681	ACTATCCCATCTCAAGAGGAGCTCAITTAAGGTTGTTGATGTGGAGGAGCAACAGCTGGAGG	4740
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4741	AGTCTGGGCGCACGATTTGACGGAAACATCTTACTTGTCCAGGCAAGATCTAGAGGGGA	4800
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4801	CCCCTTACTCGGAATCTGGAAATCAGCCTCTTCTCTGATGACCCCTGAAATCTGATCTCTCTG	4860
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4981	ATACTCTGGGTGTAATATGCAATGAGAAAGTGTGACGAGGAGAGAGCCAGAAATTTGACAG	5040
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5041	CTTCAACAGAAAGGCTCAACAAAAGATGTCCATGTGTGTGTCTGCGCTCGACCCCGAGAG	5100
5041	CTTCAACAGAAAGGCTCAACAAAAGATGTCCATGTGTGTGTCTGCGCTCGACCCCGAGAG	5100
5101	AAATTTATGCTGTGTACAGTTTGGCAGAGAAAACACACATCACTTTAACTAAATCTAAATTA	5160
5101	AAATTTATGCTGTGTACAGTTTGGCAGAGAAAACACACATCACTTTAACTAAATCTAAATTA	5160
5161	CTGAAGAGACTACTACTGTTGTTATGAAAACAGATGCTGAGTTGTGTGTGAACCGGACAC	5220
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5221	TGAATATATTTTCTAGGAATTCGGGAGGAAAAATGGGTAGTTAGCTATTTTCTGGGTGACCC	5280
5221	TGAATATATTTTCTAGGAATTCGGGAGGAAAAATGGGTAGTTAGCTATTTTCTGGGTGACCC	5280
5281	AGTCTATTAAAGAAAGAAAAATGCTGTAATGAGCATGATTTTGAAGTCAGAGAGAGATGGG	5340
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5341	TCAATGGAAGAAACCCACAGGCTCCAAAGCGGCAAGAGAAATCCAGGACACAAAAGATCT	5400
5401	TCAGGGGGCTAGAAATCTGTGTTCTATGGGCCCTTCAACCAATGCCCCACAGATCAACTGG	5460
5401	TCAGGGGGCTAGAAATCTGTGTTCTATGGGCCCTTCAACCAATGCCCCACAGATCAACTGG	5460
5461	AATGATGATGACAGCTGTGCTGTTCTGTGTGTGAAGGAGCTTTTCATCATTCACCCCTTG	5520
5461	AATGATGATGACAGCTGTGCTGTTCTGTGTGTGAAGGAGCTTTTCATCATTCACCCCTTG	5520
5521	GCAACAGGTGTCCACCCAAATTTGGTTGTGACGCGCAGATGCTGGAACAGAGGACAAATGGCT	5580
5521	GCAACAGGTGTCCACCCAAATTTGGTTGTGACGCGCAGATGCTGGAACAGAGGACAAATGGCT	5580
5581	TCCATGCAATTTGGGACAGATGTGTAGAGCACTGTGTGTGACCCGAGAGTGGGTGTGGACA	5640
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5641	GTGTAGCACTTACCAAGTCCAGAGCTGGACACTTACCTGTATCCCCAGATCCCCCACA	5700
5641	GTGTAGCACTTACCAAGTCCAGAGCTGGACACTTACCTGTATCCCCAGATCCCCCACA	5700
5701	GCCACTACTGGA	5711

Db 5701 GCCACTACTGA 5711

RESULT 12

US-08-658-322-1

; Sequence 1, Application US/08658322

; Patent No. 5869245

; GENERAL INFORMATION:

; APPLICANT: Yeung, Anthony T.

; TITLE OF INVENTION: Mismatch Endonuclease And Its Use in

; TITLE OF INVENTION: Identifying Mutations in Targeted Polynucleotide Strands

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dunn, Dorfman, Herrell and Skillman, P.C.

; STREET: 1601 Market Street, Suite 720

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19103-2307

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/658,322

; FILING DATE: 05-JUN-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Hagan, Patrick J.

; REGISTRATION NUMBER: 27,643

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 563-4100

; TELEFAX: (215) 563-4044

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5711 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: not relevant

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

US-08-658-322-1

Query Match 99.8%; Score 5701.4; DB 2; Length 5711;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 841 CCAGTAATATGATTTGAAACCACTGAGAGCGTGTGAGTGTCCAACTCTCTAACTTGGAGT 900

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5701 GCCCACTACTGA 5711
5701 GCCCACTACTGA 5711

RESULT 13
US-08-603-753D-1
; Sequence 1, Application US/08603753D
; Patent No. 5891857

GENERAL INFORMATION:
APPLICANT: HOLT, JEFFREY T.
APPLICANT: JENSEN, ROY A.
APPLICANT: PAGE, DAVID L.
APPLICANT: KING, MARY-CLAIRE
APPLICANT: SZABO, CSILLA I.
APPLICANT: JETTON, THOMAS L.
APPLICANT: ROBINSON-BENION, CHERYL L.
APPLICANT: THOMPSON, MARILYN E.
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2
TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARLES A. TAYLOR, JR.
STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
STREET: BOULEVARD
CITY: DURHAM
STATE: NORTH CAROLINA
COUNTRY: USA
ZIP: 27707
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 5.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/603,753D
FILING DATE: 20 FEB 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/373,799
FILING DATE: 17 JAN 1995
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5712
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: adult
TISSUE TYPE: female breast
CELL TYPE: ductal carcinoma in situ, invasive
CELL TYPE: breast cancer and normal breast tissue
CELL LINE: not derived from a cell line
ORGANELLE: no
IMMEDIATE SOURCE:
LIBRARY: cDNA library derived from human
CLONE: obtained using published sequence
POSITION IN GENOME:
CHROMOSOME/SEGMENT: unknown
MAP POSITION: unknown
UNITS: unknown
FEATURE:
NAME/KEY: BRCA1
LOCATION: GenBank accession no. U14680
IDENTIFICATION METHOD: microscopically directed
IDENTIFICATION METHOD: sampling and nuclease protection assay
OTHER INFORMATION: gene encoding BRCA1 protein
PUBLICATION INFORMATION:

AUTHORS: Miki, Y., et. al.
TITLE: A strong candidate gene for the breast and
TITLE: ovarian cancer susceptibility gene BRCA1.
JOURNAL: Science
VOLUME: 266
PAGES: 66-71
DATE: 1994
RELEVANT RESIDUES IN SEQ ID NO: 1:
US-08-603-753D-1

Query Match 99.8%; Score 5701.4; DB 2; Length 5712;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Qy 661 AATTGGGATCTGATTTCTTGAAGATACCGTTAATAGGCAACTTATTGCAAGTGTGGAG 720
Db 661 AATTGGGATCTGATTTCTTGAAGATACCGTTAATAGGCAACTTATTGCAAGTGTGGAG 720
Qy 721 ATCAAGAAATTTTACAAATCACCCCTCAAGGAACCGGATGAATCAGTTTGATTCG 780
Db 721 ATCAAGAAATTTTACAAATCACCCCTCAAGGAACCGGATGAATCAGTTTGATTCG 780
Qy 781 CAAAAGAGGCTCTGTGAGATTTTCTGAGAGCGGATGTAAACAATCTGACATCATCAAC 840
Db 781 CAAAAGAGGCTCTGTGAGATTTTCTGAGAGCGGATGTAAACAATCTGACATCATCAAC 840
Qy 841 CCAGTAATATGATTTTGAACCAACACTGAGAGGCTGACGCTGAGAGGATCCAGAAAGT 900
Db 841 CCAGTAATATGATTTTGAACCAACACTGAGAGGCTGACGCTGAGAGGATCCAGAAAGT 900

QY 901 ATCAGGCTAGTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCAAAATACTCATGCCA 960
DB |||||
QY 901 ATCAGGCTAGTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCAAAATACTCATGCCA 960
DB |||||
QY 961 GCTCAATACAGCATGAGAACGCGATTATTACTCACTAAGACAGAGATGAATGTAGAAA 1020
DB |||||
QY 961 GCTCAATACAGCATGAGAACGCGATTATTACTCACTAAGACAGAGATGAATGTAGAAA 1020
DB |||||
QY 1021 AGGCTGAATCTGTAAATAAAAGCAAAACAGCTGGCTTAGCAAGAGCCCAACATACAGAT 1080
DB |||||
QY 1021 AGGCTGAATCTGTAAATAAAAGCAAAACAGCTGGCTTAGCAAGAGCCCAACATACAGAT 1080
DB |||||
QY 1081 GGGCTGGAGTAAAGAACATGTAAATGATAGCGGACTCCAGACACAGAAAAAAGGTAG 1140
DB |||||
QY 1141 ATCTGAATCTGATCCCTGTTGAGAGAAAAGAAATGAATAAGCAGAAAATGCGCATGCT 1200
DB |||||
QY 1141 ATCTGAATCTGATCCCTGTTGTGAGAGAAAAGAAATGAATAAGCAGAAAATGCGCATGCT 1200
DB |||||
QY 1201 CAGAGAACTTAGAGATCTGAAGATGTTCTTGGATTAACACTAAATAGCAGCATTCAGA 1260
DB |||||
QY 1201 CAGAGAACTTAGAGATCTGAAGATGTTCTTGGATTAACACTAAATAGCAGCATTCAGA 1260
DB |||||
QY 1261 AAGTTAATGAGTGGTTTTCCAGAGAGTGAATGAATCTGTAGGTTCTGATGACTCACATGATG 1320
DB |||||
QY 1261 AAGTTAATGAGTGGTTTTCCAGAGAGTGAATGAATCTGTAGGTTCTGATGACTCACATGATG 1320
DB |||||
QY 1321 GGGAGTCTGAATCAAAATCCAAAGTAGCTGATGATTAATGGAAGTTCTTAATGAGGTAGATG 1380
DB |||||
QY 1321 GGGAGTCTGAATCAAAATCCAAAGTAGCTGATGATTAATGGAAGTTCTTAATGAGGTAGATG 1380
DB |||||
QY 1381 AATATTCTGGTTCTTCAGAGAAATAGACTTACTGGCCAGTGATCTCATGAGGCTTAA 1440
DB |||||
QY 1381 AATATTCTGGTTCTTCAGAGAAATAGACTTACTGGCCAGTGATCTCATGAGGCTTAA 1440
DB |||||
QY 1441 TATGTAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGATGAATTAAGACAAATAT 1500
DB |||||
QY 1441 TATGTAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGATGAATTAAGACAAATAT 1500
DB |||||
QY 1501 TTGGAAACCTATCGGAGAGCGAGCCCTCCCACTTAAGCATGTAACTGAAATC 1560
DB |||||
QY 1501 TTGGAAACCTATCGGAGAGCGAGCCCTCCCACTTAAGCATGTAACTGAAATC 1560
DB |||||
QY 1561 TAAATTATAGGAGCAATTTGTTACTGAGCCACAGATAATAACAGAGCGTCCCTCACAATA 1620
DB |||||
QY 1561 TAAATTATAGGAGCAATTTGTTACTGAGCCACAGATAATAACAGAGCGTCCCTCACAATA 1620
DB |||||
QY 1621 AATTAAAGGTAAGAGAGACTCATCAGGCTTCATCTGAGATTTTATCAAGAAAG 1680
DB |||||
QY 1621 AATTAAAGGTAAGAGAGACTCATCAGGCTTCATCTGAGATTTTATCAAGAAAG 1680
DB |||||
QY 1681 CAGATTTGGCAGTTCAAAAGACTCTGAAATGATAATACAGGAACTAACCAACGAGC 1740
DB |||||
QY 1681 CAGATTTGGCAGTTCAAAAGACTCTGAAATGATAATACAGGAACTAACCAACGAGC 1740
DB |||||
QY 1741 AGAATGGTCAAGTGAATATTACTAATAGTGGTCAAGCAATAAACAAGAGGTGAT 1800
DB |||||
QY 1741 AGAATGGTCAAGTGAATATTACTAATAGTGGTCAAGCAATAAACAAGAGGTGAT 1800
DB |||||
QY 1801 CTATTCAGAAATGAGAAATCTTAACCAATAGATCACTCGAAAGAAATCTGCTTCA 1860
DB |||||
QY 1801 CTATTCAGAAATGAGAAATCTTAACCAATAGATCACTCGAAAGAAATCTGCTTCA 1860
DB |||||
QY 1861 AAAAGAAAGCTGAACCTATAAGCAGCAGTATAAGCAATATGGAATCGAATTAATATCC 1920
DB |||||
QY 1861 AAAAGAAAGCTGAACCTATAAGCAGCAGTATAAGCAATATGGAATCGAATTAATATCC 1920
DB |||||
QY 1921 ACAATTCAAAGACCTTAAAGAAATAGGCTGAGAGAGATCTTCTACCGAGCATATTC 1980
DB |||||
QY 1921 ACAATTCAAAGACCTTAAAGAAATAGGCTGAGAGAGATCTTCTACCGAGCATATTC 1980
DB |||||

QY 1981 ATGGCTTGAACCTAGTAGTCAGTAGAAAATCTTAAGCCCACTTAATTTGTACTGAATTCGAAA 2040
DB |||||
QY 1981 ATGGCTTGAACCTAGTAGTCAGTAGAAAATCTTAAGCCCACTTAATTTGTACTGAATTCGAAA 2040
DB |||||
QY 2041 TTGATAGTCTGTTCTTAGCAGTGAAGAGATAAAGAAAAAAGTAACAACCAATGCGAGTCA 2100
DB |||||
QY 2041 TTGATAGTCTGTTCTTAGCAGTGAAGAGATAAAGAAAAAAGTAACAACCAATGCGAGTCA 2100
DB |||||
QY 2101 GGCACAGCAAAACCTACAACCTCAFGAAGGTAAAGAACCTGCAACTGGAGCCAAAGAGA 2160
DB |||||
QY 2101 GGCACAGCAAAACCTACAACCTCAFGAAGGTAAAGAACCTGCAACTGGAGCCAAAGAGA 2160
DB |||||
QY 2161 GTAAACAGCCCAATGAACAGCAAGTAAAGACATGACAGTGTACTTTTCCAGAGCTGA 2220
DB |||||
QY 2161 GTAAACAGCCCAATGAACAGCAAGTAAAGACATGACAGTGTACTTTTCCAGAGCTGA 2220
DB |||||
QY 2221 AGTTAAACAAATGCACTGGTCTTTTACTAAGTGTTCAAATACAGTGAACCTTAAAGAAAT 2280
DB |||||
QY 2221 AGTTAAACAAATGCACTGGTCTTTTACTAAGTGTTCAAATACAGTGAACCTTAAAGAAAT 2280
DB |||||
QY 2281 TTGTCATCTAGCTAGCTTCCAGAGAGAGAAAAGAGAGAACTAGAGAACAGTTTAAAGTGT 2340
DB |||||
QY 2281 TTGTCATCTAGCTAGCTTCCAGAGAGAGAAAAGAGAGAACTAGAGAACAGTTTAAAGTGT 2340
DB |||||
QY 2341 CTAAATATGCTGAAGACCCCAAGAGTCTCATGTTTAAAGTGAGAGAGGGTTTTGCAAACTG 2400
DB |||||
QY 2341 CTAAATATGCTGAAGACCCCAAGAGTCTCATGTTTAAAGTGAGAGAGGGTTTTGCAAACTG 2400
DB |||||
QY 2401 AAGATCTGTAGAGATGACAGTATTTTCACTGTGACTCTGTACTGTATTTGGCACTCAGG 2460
DB |||||
QY 2401 AAGATCTGTAGAGATGACAGTATTTTCACTGTGACTCTGTACTGTATTTGGCACTCAGG 2460
DB |||||
QY 2461 AAGATCTCTGTTACTGGAAGTTAGCACTCTAGGAGGCAAAAACAGAACCAATTAAT 2520
DB |||||
QY 2461 AAGATCTCTGTTACTGGAAGTTAGCACTCTAGGAGGCAAAAACAGAACCAATTAAT 2520
DB |||||
QY 2521 GTGTGAGTCAAGTGTGAGCAATTTGAAAAACCCCAAGGCACTAATTTCAATGTTTTCAAAG 2580
DB |||||
QY 2521 GTGTGAGTCAAGTGTGAGCAATTTGAAAAACCCCAAGGCACTAATTTCAATGTTTTCAAAG 2580
DB |||||
QY 2581 AATATGAAATGACACAGAGAGGCTTTAAGTATCCATTGGACATGAAGTTTAAACACAGTC 2640
DB |||||
QY 2581 AATATGAAATGACACAGAGAGGCTTTAAGTATCCATTGGACATGAAGTTTAAACACAGTC 2640
DB |||||
QY 2641 GGGAAACAAAGCATAGAAAATGGAAGAGTGAACCTGATGCTCAGTATTTCCAGAAATACAT 2700
DB |||||
QY 2641 GGGAAACAAAGCATAGAAAATGGAAGAGTGAACCTGATGCTCAGTATTTCCAGAAATACAT 2700
DB |||||
QY 2701 TCAAGGTTTCAAGAGCGCAGTCAATTTGCTCCGTTTTCAATCCAGGAAATGCAAGAGG 2760
DB |||||
QY 2701 TCAAGGTTTCAAGAGCGCAGTCAATTTGCTCCGTTTTCAATCCAGGAAATGCAAGAGG 2760
DB |||||
QY 2761 AATGTGCAACATTTCTCTGCCCACTCTGGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT 2820
DB |||||
QY 2761 AATGTGCAACATTTCTCTGCCCACTCTGGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT 2820
DB |||||
QY 2821 TTGAATGTGAACAAAGAGAGAAATCAAGGAAGATGAGTCTAATATCAAGCTGTAC 2880
DB |||||
QY 2821 TTGAATGTGAACAAAGAGAGAAATCAAGGAAGATGAGTCTAATATCAAGCTGTAC 2880
DB |||||
QY 2881 AGACAGTTAATATCATCTGCGGCTTTCTGTGTTGTGAGAAAGATAAGCCAGTTGATA 2940
DB |||||
QY 2881 AGACAGTTAATATCATCTGCGGCTTTCTGTGTTGTGAGAAAGATAAGCCAGTTGATA 2940
DB |||||
QY 2941 ATGCCAAATAGTAGTATCAAAAGAGGCTCTAGGTTTTGTCTATCATCTCAGTTCAGAGGCA 3000
DB |||||
QY 2941 ATGCCAAATAGTAGTATCAAAAGAGGCTCTAGGTTTTGTCTATCATCTCAGTTCAGAGGCA 3000
DB |||||
QY 3001 ACCGAACTGACATCTTATCCAAATTAACATGACTTTTACAAACCCCAATTCGTTATAC 3060
DB |||||
QY 3001 ACCGAACTGACATCTTATCCAAATTAACATGACTTTTACAAACCCCAATTCGTTATAC 3060
DB |||||
QY 3061 CACCACCTTTTCCCATCAAGTCAATTTGTTTAAAACTAAATGTAAGAAAAATCTCTGAGAGG 3120
DB |||||

[illegible]

4141	DB	TTTCAGATGATGAAGAAAGGAGAAACGGGCTTGGAGAGAAAATAATCAAGAGAGCAAGCA	4200
4201	QY	TGGAATTCAAACTTTAGGTGAAGACGACATCTCGGTGTGAGAGTGAACAAGCGTCTCTGAAG	4260
4201	DB	TGGAATTCAAACTTTAGGTGAAGACGACATCTCGGTGTGAGAGTGAACAAGCGTCTCTGAAG	4260
4261	QY	ACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAACTTACCCTCAGCAGAGGATACCATGC	4320
4261	DB	ACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAACTTACCCTCAGCAGAGGATACCATGC	4320
4321	QY	AACATAACCTGTATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAGCTGTGTTAGAACAGC	4380
4321	DB	AACATAACCTGTATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAGCTGTGTTAGAACAGC	4380
4381	QY	ATGGAGCGAGCCCTTTAAACAGCTACCCCTTCATCATTAAGTGACTCTTCTGCCCTTTGAGG	4440
4381	DB	ATGGAGCGAGCCCTTTAAACAGCTACCCCTTCATCATTAAGTGACTCTTCTGCCCTTTGAGG	4440
4441	QY	ACCTGCCAATTCAGAAACAAAGCACATCAGAAAAAGCAGATTATTAATTCACAGAAAGTA	4500
4441	DB	ACCTGCCAATTCAGAAACAAAGCACATCAGAAAAAGCAGATTATTAATTCACAGAAAGTA	4500
4501	QY	GTGAATACCTTATAGCCGAATTCAGAGGCGCTTCTGTGTGACAAAGTTTGAGGTGTCTG	4560
4501	DB	GTGAATACCTTATAGCCGAATTCAGAGGCGCTTCTGTGTGACAAAGTTTGAGGTGTCTG	4560
4561	QY	CAGATAGTCTACAGTAAATAAAGAACACAGAGTGGAAAGGTCATCCCTTCTTAAT	4620
4561	DB	CAGATAGTCTACAGTAAATAAAGAACACAGAGTGGAAAGGTCATCCCTTCTTAAT	4620
4621	QY	GCCCATCAITAGATGATAGTGGTACATGACACAGTTGCTCTGGAGTCTTCAGAAATAGAA	4680
4621	DB	GCCCATCAITAGATGATAGTGGTACATGACACAGTTGCTCTGGAGTCTTCAGAAATAGAA	4680
4681	QY	ACTACCCATCTCAGAGGAGCTCATTAAGGTTGTGATGTGGAGGAGCAACAGCTGGAG	4740
4681	DB	ACTACCCATCTCAGAGGAGCTCATTAAGGTTGTGATGTGGAGGAGCAACAGCTGGAG	4740
4741	QY	AGTCTGGGCGACACGATTTGACGGGAAACATCTTTACTTGGCCAGGCAAGATCTAGAGGAA	4800
4741	DB	AGTCTGGGCGACACGATTTGACGGGAAACATCTTTACTTGGCCAGGCAAGATCTAGAGGAA	4800
4801	QY	CCCCTTACCTGGAAATCTGGAAATCAGCGCTTTCTCTGATGACCCGTGAATCTGATCTCTG	4860
4801	DB	CCCCTTACCTGGAAATCTGGAAATCAGCGCTTTCTCTGATGACCCGTGAATCTGATCTCTG	4860
4861	QY	AAGACAGAGCCCGAGAGTCAAGTCTGTGGCAACATACCATCTTCAACTCTGCAATTGA	4920
4861	DB	AAGACAGAGCCCGAGAGTCAAGTCTGTGGCAACATACCATCTTCAACTCTGCAATTGA	4920
4921	QY	AAGTTCCTCCCAATTGAAAGTTGCAGAAATCTGCCAGGGTCCAGCTGCTGCTCATPACTCTG	4980
4921	DB	AAGTTCCTCCCAATTGAAAGTTGCAGAAATCTGCCAGGGTCCAGCTGCTGCTCATPACTCTG	4980
4981	QY	ATATCTGTGGTATATGCAATCGAAGAAAGTGTGAGCAGGGAGAGCCAGAAATTGACAG	5040
4981	DB	ATATCTGTGGTATATGCAATCGAAGAAAGTGTGAGCAGGGAGAGCCAGAAATTGACAG	5040
5041	QY	CTTCAACAGAAAGGGTCAACAAAGAAATCTCCATGTTGGTGTCTGGCCCTGACCCAGAG	5100
5041	DB	CTTCAACAGAAAGGGTCAACAAAGAAATCTCCATGTTGGTGTCTGGCCCTGACCCAGAG	5100
5101	QY	AATTTATGCTGTGTACAGTTTGCAGAAAAACACACATCACTTTAACTTAATCTTAATTA	5160
5101	DB	AATTTATGCTGTGTACAGTTTGCAGAAAAACACACATCACTTTAACTTAATCTTAATTA	5160
5161	QY	CTGAAGAGACTACTCATGTTGTTTATGAAACACAGATGCTCAGTTTGTGTGTGAACGACAC	5220
5161	DB	CTGAAGAGACTACTCATGTTGTTTATGAAACACAGATGCTCAGTTTGTGTGTGAACGACAC	5220
5221	QY	TGAAATATTTTCTAGGAATTCGGGAGGAAAAATGGGTAGTACTACTATTTCTGGGTGACCC	5280
5221	DB	TGAAATATTTTCTAGGAATTCGGGAGGAAAAATGGGTAGTACTACTATTTCTGGGTGACCC	5280

QY	301	GTCTTTATGTAAAGATGATATATACCAAAAGGAGCCCTACAGAAGATTAOCGAGATTTAACTC	360
DB	301	GTCTTTATGTAAAGATGATATATACCAAAAGGAGCCCTACAGAAGATTAOCGAGATTTAACTC	360
QY	361	AACTTGTTGAAGAGCTATTGGAATCATTTCTGTCTTTTCAGCTTGACACAGGTTTGAGT	420
DB	361	AACTTGTTGAAGAGCTATTGGAATCATTTCTGTCTTTTCAGCTTGACACAGGTTTGAGT	420
QY	421	ATGCAAAACAGCTATAATTTTTCAAAAAAGGAAAAATTAATCTCTCTGAACTCTAAAGAGATG	480
DB	421	ATGCAAAACAGCTATAATTTTTCAAAAAAGGAAAAATTAATCTCTCTGAACTCTAAAGAGATG	480
QY	481	AACTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCACAAAGACTTCTACAGAGTG	540
DB	481	AACTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCACAAAGACTTCTACAGAGTG	540
QY	541	AACCCGAAAAATCCTTCTCTGAGGAAACCACTCTCAGTGTCCAACTCTCTAAACCTTGGAA	600
DB	541	AACCCGAAAAATCCTTCTCTGAGGAAACCACTCTCAGTGTCCAACTCTCTAAACCTTGGAA	600
QY	601	CTGTGAGAACTCTGAGGACAGACAGCGGATACAACTCTCAAGAGACCTCTGTCTACATTC	660
DB	601	CTGTGAGAACTCTGAGGACAGACAGCGGATACAACTCTCAAGAGACCTCTGTCTACATTC	660
QY	661	AAATTGGGATCTGATTCTTCTCAAGATACCGTTTAATAAGGCAACTTTATGCAAGTGTGGCAG	720
DB	661	AAATTGGGATCTGATTCTTCTCAAGATACCGTTTAATAAGGCAACTTTATGCAAGTGTGGCAG	720
QY	721	ATCAAGAAATTTGTAACAATCAACCCCTCAAGGAAACGAGGATGAATCAGTTTGGATTCTGT	780
DB	721	ATCAAGAAATTTGTAACAATCAACCCCTCAAGGAAACGAGGATGAATCAGTTTGGATTCTGT	780
QY	781	CAAAAAAGGCTCTGTGTGAATTTCTCGACGCGATGTAAACAAATPACTGAACTCATCAAC	840
DB	781	CAAAAAAGGCTCTGTGTGAATTTCTCGACGCGATGTAAACAAATPACTGAACTCATCAAC	840
QY	841	CCAGTAATTAATGATTTGTAACCACTCAGAGACCGTGCAGCTGAGAGCATCCAGAAAAGT	900
DB	841	CCAGTAATTAATGATTTGTAACCACTCAGAGACCGTGCAGCTGAGAGCATCCAGAAAAGT	900
QY	901	ATCAGGGTAGTCTTGTTTCAAACTTGATGTGGAGCCATGTGGCACAAATPACTCATGCCA	960
DB	901	ATCAGGGTAGTCTTGTTTCAAACTTGATGTGGAGCCATGTGGCACAAATPACTCATGCCA	960
QY	961	GCTCATTTACGATGAGAAACAGCAGTTTATTACTCACTAAAGACAGAAATGAATGTAGAAA	1020
DB	961	GCTCATTTACGATGAGAAACAGCAGTTTATTACTCACTAAAGACAGAAATGAATGTAGAAA	1020
QY	1021	AGGCTGAATTTCTGTAATAAAGCAAAACAGCTTGCCTTAGCAGAGGCCAATCAACGAT	1080
DB	1021	AGGCTGAATTTCTGTAATAAAGCAAAACAGCTTGCCTTAGCAGAGGCCAATCAACGAT	1080
QY	1081	GGGCTGGAAGTAAAGAAACATGTAATGATAGGCCGACTCCAGCACAGAAAAAAGGTAG	1140
DB	1081	GGGCTGGAAGTAAAGAAACATGTAATGATAGGCCGACTCCAGCACAGAAAAAAGGTAG	1140
QY	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGAAATGGAATTAAGCAAACTGCGCATGCT	1200
DB	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGAAATGGAATTAAGCAAACTGCGCATGCT	1200
QY	1201	CAGAGAACTCTTAGAGATACTGAAGATGTTCTCTTGGATAACACTAAATAGCAGCATTCAGA	1260
DB	1201	CAGAGAACTCTTAGAGATACTGAAGATGTTCTCTTGGATAACACTAAATAGCAGCATTCAGA	1260
QY	1261	AAGTTAATGAGTGGTTTTCCAGAAAGTGAATGAATGTTAGTCTTGTGATGACTCAATGATG	1320
DB	1261	AAGTTAATGAGTGGTTTTCCAGAAAGTGAATGAATGTTAGTCTTGTGATGACTCAATGATG	1320
QY	1321	GGGAGTCTGAATCAAACTGCAATGCTGATGTAATGAGCGTTCTAAATGAGGTAGATG	1380
DB	1321	GGGAGTCTGAATCAAACTGCAATGCTGATGTAATGAGCGTTCTAAATGAGGTAGATG	1380

Qy	1381	AAATATCTGGTTCCTTCAGAGAAAATAGACTTACTGCGCAGTGAATCTCTCATGAGGCTTTAA	1444
Db	1381	AAATATCTGGTTCCTTCAGAGAAAATAGACTTACTGCGCAGTGAATCTCTCATGAGGCTTTAA	1440
Qy	1441	TATGTAAGAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATTGAAGACAAAAATAT	1500
Db	1441	TATGTAAGAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATTGAAGACAAAAATAT	1500
Qy	1501	TTGGGAAAACTATCGGAAGAGGCAAGCCTCCCAACTTAAGCCATGTAACCTGAAAATC	1560
Db	1501	TTGGGAAAACTATCGGAAGAGGCAAGCCTCCCAACTTAAGCCATGTAACCTGAAAATC	1560
Qy	1561	TAATATTAGAGCAATTTGTTTACTGAGCCAAGATATAACAAGAGCGTCCCTCACAAATA	1620
Db	1561	TAATATTAGAGCAATTTGTTTACTGAGCCAAGATATAACAAGAGCGTCCCTCACAAATA	1620
Qy	1621	AAATTAAGCGTAAAGGAGACCTACATCAGGCGCTTCATCTCGAGGATTTTATCAAGAAAG	1680
Db	1621	AAATTAAGCGTAAAGGAGACCTACATCAGGCGCTTCATCTCGAGGATTTTATCAAGAAAG	1680
Qy	1681	CAGATTGGCAGTTCAAAGCACTCCTGAAATGATAAATCAGGCAACTAACCACAAACGAGC	1740
Db	1681	CAGATTGGCAGTTCAAAGCACTCCTGAAATGATAAATCAGGCAACTAACCACAAACGAGC	1740
Qy	1741	AGATGGTCAAGTCATGAATATTACTAATAGTGGTCATGAGAAATAACAAAGGTGATT	1800
Db	1741	AGATGGTCAAGTCATGAATATTACTAATAGTGGTCATGAGAAATAACAAAGGTGATT	1800
Qy	1801	CTATTTCGAATGAGAAAAATCCTTAACCCATAGATCACTCGAAAAAGAAATCTGCTTTCA	1860
Db	1801	CTATTTCGAATGAGAAAAATCCTTAACCCATAGATCACTCGAAAAAGAAATCTGCTTTCA	1860
Qy	1861	AAACGAAGCTGAACCTATAAGCAGCAGTATAGCAATATGGAACCTCGAATTAATAATCC	1920
Db	1861	AAACGAAGCTGAACCTATAAGCAGCAGTATAGCAATATGGAACCTCGAATTAATAATCC	1920
Qy	1921	ACAAATCAAAGCACTTAATAAGAAATAGGCTGAGGAGGAAGTCTTCTTACGAGGCAATTTC	1980
Db	1921	ACAAATCAAAGCACTTAATAAGAAATAGGCTGAGGAGGAAGTCTTCTTACGAGGCAATTTC	1980
Qy	1981	ATGGCTTTGAACCTAGTAGTCAGTAGAGAACTTAAGCCCACTTAATGTTACTGAAATTCGAAA	2040
Db	1981	ATGGCTTTGAACCTAGTAGTCAGTAGAGAACTTAAGCCCACTTAATGTTACTGAAATTCGAAA	2040
Qy	2041	TTGATAGTTCTTTCTAGCAGTGAAGAGATAAAGAAAAAAAGTAGTCAACCAATGCCAGTCA	2100
Db	2041	TTGATAGTTCTTTCTAGCAGTGAAGAGATAAAGAAAAAAAGTAGTCAACCAATGCCAGTCA	2100
Qy	2101	GGCACAGCAAAACCTTACAACTCATGGAAGGTTAAGAACTCTGCAACTGAGGCCAAGAGA	2160
Db	2101	GGCACAGCAAAACCTTACAACTCATGGAAGGTTAAGAACTCTGCAACTGAGGCCAAGAGA	2160
Qy	2161	GTAACAAGCCAAATGAACAGACAAGTAAAGACATGACAGTGAATCTTCTCCAGAGCTGA	2220
Db	2161	GTAACAAGCCAAATGAACAGACAAGTAAAGACATGACAGTGAATCTTCTCCAGAGCTGA	2220
Qy	2221	AGTTAACAATGCACTGGTCTTTTCTAATGTTGTTCAATACACAGTGAACCTTAAGAAT	2280
Db	2221	AGTTAACAATGCACTGGTCTTTTCTAATGTTGTTCAATACACAGTGAACCTTAAGAAT	2280
Qy	2281	TTGTCAATCTAGCCTTCCAAAGAGAGAAAGAGAGAAACTPAGAAAACAGTTTAAAGTGT	2340
Db	2281	TTGTCAATCTAGCCTTCCAAAGAGAGAAAGAGAGAAACTPAGAAAACAGTTTAAAGTGT	2340
Qy	2341	CTAATAATGTCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAAGGTTTTTCAAAACCTG	2400
Db	2341	CTAATAATGTCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAAGGTTTTTCAAAACCTG	2400
Qy	2401	AAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACTCGTACTGATATGGCACCTCAGG	2460
Db	2401	AAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACTCGTACTGATATGGCACCTCAGG	2460
Qy	2461	AAAGTATCTCGTTACTGGAGTTTAGCACTCTAGGGAGGCAAAAACAGAACCAAAATAAT	2520

Db 2461 AAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGACACCAATATAAT 2520
Qy |||||
Db 2521 GTGTGAGTCAGTGTGTCAGCAATTTGAAAACCCCAAGGAGCTAAATTCATGTTGTTCCAAAG 2580
Qy |||||
Db 2521 GTGTGAGTCAGTGTGTCAGCAATTTGAAAACCCCAAGGAGCTAAATTCATGTTGTTCCAAAG 2580
Qy |||||
Db 2581 ATAATAGAAATGACACAGAGAGGCTTTAAAGTATCCATTTGGGACATGAAGTTAAACACAGTC 2640
Qy |||||
Db 2581 ATAATAGAAATGACACAGAGGCTTTAAAGTATCCATTTGGGACATGAAGTTAAACACAGTC 2640
Qy |||||
Db 2641 GGGAAACAGCAGTAAATGGAAGAAAGTGAATGATGCTCAATTTGCGAGATATCAT 2700
Qy |||||
Db 2641 GGGAAACAGCAGTAAATGGAAGAAAGTGAATGATGCTCAATTTGCGAGATATCAT 2700
Qy |||||
Db 2701 TCAAGGTTTCAAAGCCGAGTCATTTGCTCTGTTTCAAATCCAGGAAATCCAGAGAGG 2760
Qy |||||
Db 2701 TCAAGGTTTCAAAGCCGAGTCATTTGCTCTGTTTCAAATCCAGGAAATCCAGAGAGG 2760
Qy |||||
Db 2761 AATGTGCAACATTTCTGCCCCACTCTGGGTCCTTTAAAGAAACAAAGTCCAAAGTCACTT 2820
Qy |||||
Db 2761 AATGTGCAACATTTCTGCCCCACTCTGGGTCCTTTAAAGAAACAAAGTCCAAAGTCACTT 2820
Qy |||||
Db 2821 TTGAATGTGAACAAGAGAAATCAAGGAAGATGAGTCTAAATATCAAGCTGTAC 2880
Qy |||||
Db 2821 TTGAATGTGAACAAGAGAAATCAAGGAAGATGAGTCTAAATATCAAGCTGTAC 2880
Qy |||||
Db 2881 AGACAGTTAATATCACTCGAGGCTTTCTGTTGGTGGTTCAGAGAGATAAGCCAGTTGATA 2940
Qy |||||
Db 2881 AGACAGTTAATATCACTCGAGGCTTTCTGTTGGTGGTTCAGAGAGATAAGCCAGTTGATA 2940
Qy |||||
Db 2941 ATGCCAATGTAGTATGAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGCA 3000
Qy |||||
Db 2941 ATGCCAATGTAGTATGAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGCA 3000
Qy |||||
Db 3001 ACBAACCTGGACTCAATTAACCAATGAGGCTTTTACAAAACCCATATCGTATAC 3060
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Scoring table: IDENTITY NUC
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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

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ALIGNMENTS

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DEFINITION Sequence 5 from patent US 5750400.
ACCESSION AR007335
VERSION AR007335.1 GI:3966819
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5711)
AUTHORS Murphy, P.D., Allen, A.C., Alvares, C.P., Critz, B.S., Olson, S.J.,
Schelker, D.B. and Zeng, B.
TITLE Coding sequences of the human BRCA1 gene
JOURNAL Patent: US 5750400-A 5 12-MAY-1998;

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Best Local Similarity		100.0%; Pred. No. 0;					
Matches 571; Conservative		0; Mismatches 0; Indels 0; Gaps 0;					
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Qy	481	AAGTTCTCATCATCAAAAGTGGCTACAGAAACCGGCCAAAGAGCTTCTACAGAGTG	540	Qy	1441	TATGTTAAAGTGAAGAGTTCCTCCAAATCAGTAGAGATTAATTTGAAGACAAAATAT	1500
Db	481	AAGTTCTCATCATCAAAAGTGGCTACAGAAACCGGCCAAAGAGCTTCTACAGAGTG	540	Db	1441	TATGTTAAAGTGAAGAGTTCCTCCAAATCAGTAGAGATTAATTTGAAGACAAAATAT	1500
Qy	541	AACCGGAAATCTTCTTTCAGGAAACCAAGTCTCAGTGTCCAACTCTCTAACTTGGAA	600	Qy	1501	TTGGGAAACCTATCGGAGAGGAGGAGCTCCCACTTANGCCATGTAACTGAAATC	1560
Db	541	AACCGGAAATCTTCTTTCAGGAAACCAAGTCTCAGTGTCCAACTCTCTAACTTGGAA	600	Db	1501	TTGGGAAACCTATCGGAGAGGAGGAGCTCCCACTTANGCCATGTAACTGAAATC	1560
Qy	601	CTGTGAGAACTCTGAGGACCAAGCAGCGATACACCTCAAAAGAGCTGTCTACATTTG	660	Qy	1561	TAATTTAGGAGCATTTGTTTACTGAGCCACAGATAATACAGAGCGTCCCTCACAAATA	1620
Db	601	CTGTGAGAACTCTGAGGACCAAGCAGCGATACACCTCAAAAGAGCTGTCTACATTTG	660	Db	1561	TAATTTAGGAGCATTTGTTTACTGAGCCACAGATAATACAGAGCGTCCCTCACAAATA	1620
Qy	661	AATTTGGATCTGATTTCTTCTGAGATACCGTTAATAGGCACTTATTTGCAAGTGTGGAG	720	Qy	1621	AATTAAGCGTAAAGAGGAGCTACATCAGCGCTTCTCATCTGAGGATTTTATCAAGAAAG	1680
Db	661	AATTTGGATCTGATTTCTTCTGAGATACCGTTAATAGGCACTTATTTGCAAGTGTGGAG	720	Db	1621	AATTAAGCGTAAAGAGGAGCTACATCAGCGCTTCTCATCTGAGGATTTTATCAAGAAAG	1680
Qy	721	ATCAAGAAATTTGTACAAATCACCCCTCAAGGACCAAGGATGAATATCAGTTTGGATTCG	780	Qy	1681	CAGATTGGCAGTTTCAAAAGACTCTCTGAAATGATAAATCAGGAACTAACCAAAACGAGC	1740
Db	721	ATCAAGAAATTTGTACAAATCACCCCTCAAGGACCAAGGATGAATATCAGTTTGGATTCG	780	Db	1681	CAGATTGGCAGTTTCAAAAGACTCTCTGAAATGATAAATCAGGAACTAACCAAAACGAGC	1740
Qy	781	CAAAAAGGCTGCTGTGAAATTTTCTGAGACGATGTAACAAATTAATTAATTAATTAAT	840	Qy	1741	AGAATGGTCAAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1800
Db	781	CAAAAAGGCTGCTGTGAAATTTTCTGAGACGATGTAACAAATTAATTAATTAATTAAT	840	Db	1741	AGAATGGTCAAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1800
Qy	841	CCAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	900	Qy	1801	CTATTTCAGATGAGAAAAATCCCTAACCCATAGATCACTCCGAAAAAGAAATCTGCTTTCA	1860
Db	841	CCAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	900	Db	1801	CTATTTCAGATGAGAAAAATCCCTAACCCATAGATCACTCCGAAAAAGAAATCTGCTTTCA	1860
Qy	901	ATCAGGTTAGTCTGTTTCAACTGATGTGGAGCTATGTGGACAAATTAATTAATTAAT	960	Qy	1861	AAACGAAAGCTGAACCTTAAAGCAGAGTATAAGCAATATGAACTCGAAATTAATATCC	1920
Db	901	ATCAGGTTAGTCTGTTTCAACTGATGTGGAGCTATGTGGACAAATTAATTAATTAAT	960	Db	1861	AAACGAAAGCTGAACCTTAAAGCAGAGTATAAGCAATATGAACTCGAAATTAATATCC	1920
Qy	961	ATCAGGTTAGTCTGTTTCAACTGATGTGGAGCTATGTGGACAAATTAATTAATTAAT	1020	Qy	1921	ACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1980
Db	961	ATCAGGTTAGTCTGTTTCAACTGATGTGGAGCTATGTGGACAAATTAATTAATTAAT	1020	Db	1921	ACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1980
Qy	1021	ATCAGGTTAGTCTGTTTCAACTGATGTGGAGCTATGTGGACAAATTAATTAATTAAT	1080	Qy	1981	ATCGGCTTGAACCTAGTAGTCAGTAGAATCTTAAGCCCACTTAATTTGACTGAATTCGAA	2040
Db	1021	ATCAGGTTAGTCTGTTTCAACTGATGTGGAGCTATGTGGACAAATTAATTAATTAAT	1080	Db	1981	ATCGGCTTGAACCTAGTAGTCAGTAGAATCTTAAGCCCACTTAATTTGACTGAATTCGAA	2040

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Db 2041 TTGATAGTGTCTTAGCAGTGAAGAGATAAGAAAAAAGAGTACAAACAAATGCCAGTCA 2100
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Db 2101 GGCAACAGCAAACTCACTCACTGAGAGTAAAGAACTGCAACTGGAGCCAAAGAGA 2160
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Db 2161 GTAAACAAGCCAAATGAACAGACAAAGTAAAGACATGACAGTATCTTCCAGAGCTGA 2220
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Db 2221 AGTTAAACAAGTCACTGCTCTTCTTACTAAGTGTCAAAATACAGTGAATCTTAAAGAT 2280
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Db 2281 TTGTCAATCTTAGCCTTCCAGAGAGAAAGAAAGAGAACTAGAAACAGTTTAAAGTGT 2340
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DB 301 GTCCCTTTATGTAGAAATGATATAAACCAGAGAGGCTTACAGAAAGTAGCAGATTTAGTC 360
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DB 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAGAGCGTCTGTCTACATG 660
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Db
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ACCESSION AR112808
VERSION AR112808.1 GI:14092708
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SOURCE Unknown.
ORGANISM Unknown.
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Thurber, D., and Zeng, B.
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Qy	2881	AGACAGTTAATATCACTGACAGGCTTCTGCTGGTCTGAGAAAGATTAAGCAGTGTGATA	2940
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Qy	3061	CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAAATGTTAGAAATCTCTCTAGAGG	3120
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RESULT 5
LOCUS 159546 5711 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 1 from patent US 5654155.
ACCESSION 159546
VERSION 159546.1 GI:2478178
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5711)
AUTHORS Murphy, P.D., Allen, A.C., Alvares, C.P., Critz, B.S., Olson, S.J.,
Scheller, D.B. and Zeng, B.
TITLE Consensus sequence of the human BRCA1 gene
JOURNAL Patent: US 5654155-A 1 05-AUG-1997;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 5709.4; DB 6; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Unclassified.	
REFERENCE 1 (bases 1 to 5711)	
AUTHORS Murphy, P.D., Allen, A.C., Alvares, C.P., Critz, B.S., Olson, S.J., Schelter, D.B. and Zeng, B.	
TITLE Coding sequences of the human BRCA1 gene	
JOURNAL Patent: US 5750400-A 3 12-MAY-1998;	
FEATURES	
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Best Local Similarity	99.9%; Pred. No. 0;
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DEFINITION Sequence 1 from patent US 5869245.
ACCESSION AR033056
VERSION AR033056.1 GI:5948661
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 5711)
AUTHORS Yeung, A.T.
TITLE Mismatch endonuclease and its use in identifying mutations in
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JOURNAL Patent: US 5869245-A 1 09-FEB-1999;
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LOCUS Homo sapiens breast and ovarian cancer susceptibility (BRCA1) mRNA,
DEFINITION complete cds.
ACCESSION U14680
VERSION U14680.1 GI:555931
KEYWORDS
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 5711)
AUTHORS Miki,Y., Swensen,J., Shattuck-Eidens,D., Futreal,P.A., Harshman,K.,
Tavtigian,S., Liu,Q., Cochran,C., Bennett,L.M., Ding,W., Bell,I.,
Rosenthal,J., Hussey,C., Tran,T., McClure,M., Frye,C., Hattier,T.,
Phelps,R., Haugen-Strano,A., Katcher,H., Yakumo,K., Gholami,Z.,
Shaffer,D., Stone,S., Bayer,S., Wray,C., Bogden,R., Dayananth,P.,
Ward,J., Tonin,P., Narod,S., Bristow,P.K., Norris,F.H.,
Helvering,L., Morrison,P., Rostock,P., Lai,M., Barrett,J.C.,
Lewis,C., Neuhausen,S., Cannon-Albright,L., Goldgar,D., Wiseman,R.,
Kamb,A. and Skolnick,M.H.
TITLE A strong candidate for the breast and ovarian cancer susceptibility
gene BRCA1
JOURNAL Science 266 (5182), 66-71 (1994)
MEDLINE 95025896
PUBMED 7545954
REFERENCE 2 (bases 1 to 5711)
AUTHORS Skolnick,M.H.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-1994) Mark H. Skolnick, Myriad Genetics Inc. and
the University of Utah, 421 Wakara Way, Suite 201, Salt Lake City,
UT 84108, USA

FEATURES
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RESULT 11

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DEFINITION Sequence 1 from patent US 5891857.
ACCESSION AR070223
VERSION AR070223.1 GI:7221111
KEYWORDS Unknown.

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REFERENCE	Unclassified.
AUTHORS	1. (bases 1 to 5712) Holt, J.T., Jensen, R.A., King, M.-C., Page, D.L., Szabo, C.I., Jeton, T.L., Robinson-Benion, C.L., and Thompson, M.E.
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DB	1381 AATATTCTGCTTCTTCAAGAGAAATAGACTTCTGCGCAGTGTATCTCATGAGGCTTTAA 1440
QY	1441 TATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGATTAATATTGAAGACAAATAT 1500
DB	1441 TATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGATTAATATTGAAGACAAATAT 1500
QY	1501 TTGGGAAACCTTATCGGAAGAGGAGCCCTCCCAACTTAAAGCCATGTAACGTGAATC 1560
DB	1501 TTGGGAAACCTTATCGGAAGAGGAGCCCTCCCAACTTAAAGCCATGTAACGTGAATC 1560
QY	1561 TAATTATAGGAGCAATTTGTTTACTGAGCCACAGATAATACAGAGCGTCCCTCACAATA 1620
DB	1561 TAATTATAGGAGCAATTTGTTTACTGAGCCACAGATAATACAGAGCGTCCCTCACAATA 1620
QY	1621 AATTAAAGCTTAAAGAGACCTTACATCAGGCTTCTATCTGAGGATTTTATCAGAAAG 1680
DB	1621 AATTAAAGCTTAAAGAGACCTTACATCAGGCTTCTATCTGAGGATTTTATCAGAAAG 1680
QY	1681 CAGATTGGCAGTTTCAAAAGACTCTCTGAAATGATAAATCAAGGAACTTAAACCAACGGAGC 1740
DB	1681 CAGATTGGCAGTTTCAAAAGACTCTCTGAAATGATAAATCAAGGAACTTAAACCAACGGAGC 1740
QY	1741 AGAATGGTCAAGTGAATTAATTAATAGTGGTCAATGAGATAAATAAAGGTTGAT 1800
DB	1741 AGAATGGTCAAGTGAATTAATTAATAGTGGTCAATGAGATAAATAAAGGTTGAT 1800
QY	1801 CTATTGAGATGAGAAATCTTAACCAATCAATCACTCGAAAGAAATCTGCTTTCA 1860
DB	1801 CTATTGAGATGAGAAATCTTAACCAATCAATCACTCGAAAGAAATCTGCTTTCA 1860
QY	1861 AAAAGGAGCTGCTGAAATTTCTGAGAAGGATGTAACAAATCTGAACTCGAATTAATATCC 1920
DB	1861 AAAAGGAGCTGCTGAAATTTCTGAGAAGGATGTAACAAATCTGAACTCGAATTAATATCC 1920